

Filed: January 11, 2002 Atty. Docket No.: 015389-002640US
Applicant: Thomas R. Cech et al.
Title: HUMAN TELOMERASE CATALYTIC SUBUNIT:
DIAGNOSTIC AND THERAPEUTIC METHODS
COPY OF SEQUENCE LISTING
FROM PARENT APPLICATION NO. 08/912,951

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
- (ii) TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
- (iii) NUMBER OF SEQUENCES: 335
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESS: Townsend and Townsend and Crew LLP
 - (B) STREET: Two Embarcadero Center, 8th Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: United States of America
 - (F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/912,951
 - (B) FILING DATE: 14-AUG-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/854,050
 - (B) FILING DATE: 09-MAY-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/851,843
 - (B) FILING DATE: 06-MAY-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/846,017
 - (B) FILING DATE: 25-APR-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/844,419
 - (B) FILING DATE: 18-APR-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/724,643
 - (B) FILING DATE: 01-OCT-1996
 - (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Apple, Randolph T.
- (B) REGISTRATION NUMBER: 36,429
- (C) REFERENCE/DOCKET NUMBER: 015389-002600US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..3454
- (D) OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG 58
Met
1

CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC 106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
5 10 15

TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC 154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
20 25 30

CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG 202
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
35 40 45

CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC 250
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
50 55 60 65

CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG 298
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
70 75 80

GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG 346
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu
85 90 95

GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG 394
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu
100 105 110

GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CCG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu 275 280 285	922
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala 290 295 300 305	970
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355	1162

355					360					365						
CCC	TGG	ATG	CCA	GGG	ACT	CCC	CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	1210
Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	
370					375					380					385	
TAC	TGG	CAA	ATG	CGG	CCC	CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	1258
Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
				390					395					400		
CAG	TGC	CCC	TAC	GGG	GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	1306
Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
			405					410					415			
GCG	GTC	ACC	CCA	GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	1354
Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
		420				425						430				
TCT	GTG	GCG	GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	1402
Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
	435				440						445					
CAG	CTG	CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	1450
Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
450				455					460						465	
CGG	GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	1498
Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
			470					475						480		
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	CTG	1546
His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
		485					490					495				
GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	ATG	AGC	1594
Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
	500					505						510				
GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
	515				520						525					
CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
530				535						540					545	
CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
			550						555					560		
TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
			565				570					575				
AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
		580				585						590				
AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
	595					600					605					

CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
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GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860	2650

850		855		860		865	
TTG GTG GAT GAT TTC	TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA	2698					
Leu Val Asp Asp Phe	Leu Leu Val Thr Pro His Leu Thr His Ala Lys						
	870 875 880						
ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG	2746						
Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val							
	885 890 895						
GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC	2794						
Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala							
	900 905 910						
CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC	2842						
Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro							
	915 920 925						
TGG TGC GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC	2890						
Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp							
	930 935 940 945						
TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC	2938						
Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn							
	950 955 960						
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC	2986						
Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val							
	965 970 975						
TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC	3034						
Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser							
	980 985 990						
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG	3082						
Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln Ala							
	995 1000 1005						
TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT	3130						
Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val							
	1010 1015 1020 1025						
TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC	3178						
Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser							
	1030 1035 1040						
CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC GCA GGG ATG TCG CTG GGG	3226						
Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly							
	1045 1050 1055						
GCC AAG GGC GCC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG	3274						
Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu							
	1060 1065 1070						
TGC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC	3322						
Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr							
	1075 1080 1085						
GTG CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG	3370						
Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg							
	1090 1095 1100 1105						

AAG CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG	3418
Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro	
1110 1115 1120	
GCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCACAG	3471
Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp	
1125 1130	
CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA	3531
GGGGCGGCCC ACACCCAGGC CCGCACCCTG GGGAGTCTGA GGCCTGAGTG AGTGTTTGGC	3591
CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCAG	3651
CCAAGGGCTG AGTGTCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC	3711
TCCACCCCAG GGCCAGCTTT TCCTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTCGCC ATTGTTTACC CCTCGCCCTG CCCTCCTTTG CTTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAAT ACTGAATATA TGAGTTTTTC AGTTTTGAAA	4011
AAAA	4015

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser	
1 5 10 15	
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly	
20 25 30	
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg	
35 40 45	
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro	
50 55 60	
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu	
65 70 75 80	
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val	
85 90 95	
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro	
100 105 110	
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr	

115					120					125					
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val
130						135					140				
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val
145					150					155					160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr
				165					170					175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly
			180					185					190		
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg
			195				200					205			
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg
	210					215					220				
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg
225					230					235					240
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp
				245					250					255	
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val
			260					265					270		
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala
			275				280					285			
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His
			290			295					300				
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro
305					310					315					320
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly
				325					330					335	
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro
			340					345					350		
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser
			355				360					365			
Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln
	370					375					380				
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His
385					390					395				400	
Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg
				405					410					415	
Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln
			420				425					430			
Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu
			435			440						445			

Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	
450						455					460					
Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	
465					470					475					480	
Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	
				485					490					495		
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	
			500					505					510			
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	
		515					520					525				
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	
	530					535					540					
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	
545					550					555					560	
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	
				565					570					575		
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	
			580					585					590			
Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	
		595					600					605				
His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	
	610					615					620					
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	
625					630					635					640	
Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	
				645				650						655		
Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	
			660					665					670			
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	
		675					680					685				
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	
	690					695					700					
Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	
705					710					715					720	
Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	
				725				730						735		
Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	
			740					745					750			
Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	
		755					760					765				
Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	
	770					775					780					

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2176
- (D) OTHER INFORMATION: /note= "clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCAAGTTC CTGCACTGGC TGATGAGTGT GTACGTCGTC GAGCTGCTCA GGTCTTTCTT	60
TTATGTCACG GAGACCACGT TTCAAAGAA CAGGCTCTTT TTCTACCGGA AGAGTGTCTG	120
GAGCAAGTTG CAAAGCATTG GAATCAGACA GCACTTGAAG AGGGTGCAGC TCGGGGAGCT	180
GTCGGAAGCA GAGGTCAGGC AGCATCGGGA AGCCAGGCCG GCCCTGCTGA CGTCCAGACT	240
CCGCTTCATC CCCAAGCCTG ACGGGCTGCG GCCGATTGTG AACATGGACT ACGTCGTGGG	300
AGCCAGAACG TTCCGCAGAG AAAAGAGGGC CGAGCGTCTC ACCTCGAGGG TGAAGGCACT	360
GTTTCAGCGTG CTCAACTACG AGCGGGCGCG GCGCCCCGCG CTCCTGGGCG CCTCTGTGCT	420
GGGCCTGGAC GATATCCACA GGGCCTGGCG CACCTTCGTG CTGCGTGTGC GGGCCCAGGA	480
CCCGCCGCCT GAGCTGTACT TTGTCAAGGT GGATGTGACG GGCGCGTACG ACACCATCCC	540
CCAGGACAGG CTCACGGAGG TCATCGCCAG CATCATCAAA CCCCAGAACA CGTACTGCGT	600
GCGTCGGTAT GCCGTGGTCC AGAAGGCCGC CCATGGGCAC GTCCGCAAGG CCTTCAAGAG	660
CCACGTCCTA CGTCCAGTGC CAGGGGATCC CGCAGGGCTC CATCCTCTCC ACGCTGCTCT	720
GCAGCCTGTG CTACGGCGAC ATGGAGAACA AGCTGTTTGC GGGGATTTCG CGGGACGGGC	780
TGCTCCTGCG TTTGGTGGAT GATTTCCTGT TGGTGACACC TCACCTCACC CACGCGAAAA	840
CCTTCCTCAG GACCCTGGTC CGAGGTGTCC CTGAGTATGG CTGCGTGGTG AACTTGCGGA	900
AGACAGTGGT GAACTTCCCT GTAGAAGACG AGGCCCTGGG TGGCACGGCT TTTGTTTACA	960
TGCCGGCCCA CGGCCTATTG CCCTGGTGCG GCCTGCTGCT GGATACCCGG ACCCTGGAGG	1020
TGCAGAGCGA CTAATCCAGC TATGCCCCGA CCTCCATCAG AGCCAGTCTC ACCTTCAACC	1080
GCGGCTTCAA GGCTGGGAGG AACATGCGTC GCAAACTCTT TGGGGTCTTG CGGCTGAAGT	1140
GTACAGCCT GTTTCTGGAT TTGCAGGTGA ACAGCCTCCA GACGGTGTGC ACCAACATCT	1200

ACAAGATCCT CCTGCTGCAG GCGTACAGGT TTCACGCATG TGTGCTGCAG CTCCCATTTC	1260
ATCAGCAAGT TTGGAAGAAC CCCACATTTT TCCTGCGCGT CATCTCTGAC ACGGCCTCCC	1320
TCTGCTACTC CATCCTGAAA GCCAAGAACG CAGGGATGTC GCTGGGGGCC AAGGGCGCCG	1380
CCGGCCNTCT GCCCTCCGAG GCCGTGCAGT GGCTGTGCCA CCAAGCATTG CTGCTCAAGC	1440
TGACTCGACA CCGTGTCAAC TACGTGCCAC TCCTGGGGTC ACTCAGGACA GCCCAGACGC	1500
AGCTGAGTCG GAAGCTCCCG GGGACGACGC TGAAGTCCCT GGAGGCCGCA GCCAACCCGG	1560
CACTGCCCTC AGACTTCAAG ACCATCCTGG ACTGATGGCC ACCCGCCCAC AGCCAGGCCG	1620
AGAGCAGACA CCAGCAGCCC TGTCACGCCG GGCTCTACGT CCCAGGGAGG GAGGGGCGGC	1680
CCACACCCAG GCCTGCACCG CTGGGAGTCT GAGGCCTGAG TGAGTGTTTG GCCGAGGCCT	1740
GCATGTCCCG CTGAAGGCTG AGTGTCCGGC TGAGGCCTGA GCGAGTGTCC AGCCAAGGGC	1800
TGAGTGTTCA GCACACCTGC CGTCTTCACT TCCCCACAGG CTGGCGCTCG GCTCCACCCC	1860
AGGGCCAGCT TTTCCTCACC AGGAGCCCGG CTTCCACTCC CCACATAGGA ATAGTCCATC	1920
CCCAGATTCG CCATTGTTCA CCCCTCGCCC TGCCCTCCTT TGCCTTCCAC CCCCACCATC	1980
CAGGTGGAGA CCCTGAGAAG GACCCTGGGA GCTCTGGGAA TTTGGAGTGA CCAAAGGTGT	2040
GCCCTGTACA CAGGCGAGGA CCCTGCACCT GGATGGGGGT CCCTGTGGGT CAAATTGGGG	2100
GGAGGTGCTG TGGGAGTAAA ATACTGAATA TATGAGTTTT TCAGTTTTGN AAAAAAAAAA	2160
AAAAAAAAAA AAAAAA	2176

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3855
- (D) OTHER INFORMATION: /note= "nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..2479
- (D) OTHER INFORMATION: /product= "delta-182 variant polypeptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCAGCGCTGC	GTCTGTCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58
						Met	
						1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC	106						
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His							
5 10 15							
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC	154						
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro							
20 25 30							
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG	202						
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala							
35 40 45							
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC	250						
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro							
50 55 60 65							
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG	298						
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val							
70 75 80							
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG	346						
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu							
85 90 95							
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG	394						
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu							
100 105 110							
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC	442						
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp							
115 120 125							
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC	490						
Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly							
130 135 140 145							
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG	538						
Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu							
150 155 160							
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG	586						
Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln							
165 170 175							
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC	634						
Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro							
180 185 190							
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG	682						
Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu							
195 200 205							
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG	730						
Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly							
210 215 220 225							
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC	778						
Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly							

230										235					240					
GCT Ala	GCC Ala	CCT Pro	GAG Glu 245	CCG Pro	GAG Glu	CGG Arg	ACG Thr	CCC Pro 250	GTT Val	GGG Gly	CAG Gln	GGG Gly	TCC Ser 255	TGG Trp	GCC Ala	826				
CAC His	CCG Pro	GGC Gly 260	AGG Arg	ACG Thr	CGT Arg	GGA Gly	CCG Pro 265	AGT Ser	GAC Asp	CGT Arg	GGT Gly	TTC Phe 270	TGT Cys	GTG Val	GTG Val	874				
TCA Ser	CCT Pro 275	GCC Ala	AGA Arg	CCC Pro	GCC Ala	GAA Glu 280	GAA Glu	GCC Ala	ACC Thr	TCT Ser	TTG Leu 285	GAG Glu	GGT Gly	GCG Ala	CTC Leu	922				
TCT Ser 290	GGC Gly	ACG Thr	CGC Arg	CAC His	TCC Ser 295	CAC His	CCA Pro	TCC Ser	GTG Val	GGC Gly 300	CGC Arg	CAG Gln	CAC His	CAC His	GCG Ala 305	970				
GGC Gly	CCC Pro	CCA Pro	TCC Ser	ACA Thr 310	TCG Ser	CGG Arg	CCA Pro	CCA Pro	CGT Arg 315	CCC Pro	TGG Trp	GAC Asp	ACG Thr	CCT Pro 320	TGT Cys	1018				
CCC Pro	CCG Pro	GTG Val	TAC Tyr 325	GCC Ala	GAG Glu	ACC Thr	AAG Lys	CAC His 330	TTC Phe	CTC Leu	TAC Tyr	TCC Ser	TCA Ser 335	GGC Gly	GAC Asp	1066				
AAG Lys	GAG Glu 340	CAG Gln	CTG Leu	CGG Arg	CCC Pro	TCC Ser	TTC Phe 345	CTA Leu	CTC Leu	AGC Ser	TCT Ser	CTG Leu 350	AGG Arg	CCC Pro	AGC Ser	1114				
CTG Leu 355	ACT Thr	GGC Gly	GCT Ala	CGG Arg	AGG Arg	CTC Leu 360	GTG Val	GAG Glu	ACC Thr	ATC Ile	TTT Phe 365	CTG Leu	GGT Gly	TCC Ser	AGG Arg	1162				
CCC Pro 370	TGG Trp	ATG Met	CCA Pro	GGG Gly 375	ACT Thr	CCC Pro	CGC Arg	AGG Arg	TTG Leu 380	CCC Pro	CGC Arg	CTG Leu	CCC Pro	CAG Gln 385	CGC Arg	1210				
TAC Tyr	TGG Trp	CAA Gln	ATG Met	CGG Arg 390	CCC Pro	CTG Leu	TTT Phe	CTG Leu	GAG Glu 395	CTG Leu	CTT Leu	GGG Gly	AAC Asn	CAC His 400	GCG Ala	1258				
CAG Gln	TGC Cys	CCC Pro	TAC Tyr 405	GGG Gly	GTG Val	CTC Leu	CTC Leu	AAG Lys 410	ACG Thr	CAC His	TGC Cys	CCG Pro	CTG Leu 415	CGA Arg	GCT Ala	1306				
GCG Ala	GTC Val	ACC Thr 420	CCA Pro	GCA Ala	GCC Ala	GGT Gly	GTC Val 425	TGT Cys	GCC Ala	CGG Arg	GAG Glu	AAG Lys 430	CCC Pro	CAG Gln	GGC Gly	1354				
TCT Ser	GTG Val 435	GCG Ala	GCC Ala	CCC Pro	GAG Glu	GAG Glu 440	GAG Glu	GAC Asp	ACA Thr	GAC Asp	CCC Pro 445	CGT Arg	CGC Arg	CTG Leu	GTG Val	1402				
CAG Gln 450	CTG Leu	CTC Leu	CGC Arg	CAG Gln	CAC His 455	AGC Ser	AGC Ser	CCC Pro	TGG Trp	CAG Gln 460	GTG Val	TAC Tyr	GGC Gly	TTC Phe	GTG Val 465	1450				
CGG Arg	GCC Ala	TGC Cys	CTG Leu	CGC Arg 470	CGG Arg	CTG Leu	GTG Val	CCC Pro	CCA Pro 475	GGC Gly	CTC Leu	TGG Trp	GGC Gly	TCC Ser 480	AGG Arg	1498				

CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485 490 495	1546
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515 520 525	1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530 535 540 545	1690
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550 555 560	1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg 565 570 575	1786
AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580 585 590	1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn	2266

725										730					735					
ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC	GCC	CAT	GGG	2314				
Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly					
		740					745					750								
CAC	GTC	CGC	AAG	GCC	TTC	AAG	AGC	CAC	GTC	CTA	CGT	CCA	GTG	CCA	GGG	2362				
His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Leu	Arg	Pro	Val	Pro	Gly					
	755					760					765									
GAT	CCC	GCA	GGG	CTC	CAT	CCT	CTC	CAC	GCT	GCT	CTG	CAG	CCT	GTG	CTA	2410				
Asp	Pro	Ala	Gly	Leu	His	Pro	Leu	His	Ala	Ala	Leu	Gln	Pro	Val	Leu					
	770				775				780						785					
CGG	CGA	CAT	GGA	GAA	CAA	GCT	GTT	TGC	GGG	GAT	TCG	GCG	GGA	CGG	GCT	2458				
Arg	Arg	His	Gly	Glu	Gln	Ala	Val	Cys	Gly	Asp	Ser	Ala	Gly	Arg	Ala					
			790						795					800						
GCT	CCT	GCG	TTT	GGT	GGA	TGATTTCTTG	TTGGTGACAC	CTCACCTCAC								2506				
Ala	Pro	Ala	Phe	Gly	Gly															
			805																	
CCACGCGAAA	ACCTTCCTCA	GGACCCTGGT	CCGAGGTGTC	CCTGAGTATG	GCTGCGTGGT											2566				
GAACCTTGCGG	AAGACAGTGG	TGAACTTCCC	TGTAGAAGAC	GAGGCCCTGG	GTGGCACGGC											2626				
TTTTGTTCAG	ATGCCGGCCC	ACGGCCTATT	CCCCTGGTGC	GGCCTGCTGC	TGGATACCCG											2686				
GACCCTGGAG	GTGCAGAGCG	ACTACTCCAG	CTATGCCCCG	ACCTCCATCA	GAGCCAGTCT											2746				
CACCTTCAAC	CGCGGCTTCA	AGGCTGGGAG	GAACATGCGT	CGCAAACCTCT	TTGGGGTCTT											2806				
GCGGCTGAAG	TGTCACAGCC	TGTTTCTGGA	TTTGCAGGTG	AACAGCCTCC	AGACGGTGTG											2866				
CACCAACATC	TACAAGATCC	TCCTGCTGCA	GGCGTACAGG	TTTCACGCAT	GTGTGCTGCA											2926				
GCTCCCATTT	CATCAGCAAG	TTTGGAAGAA	CCCCACATTT	TTCCTGCGCG	TCATCTCTGA											2986				
CACGGCCTCC	CTCTGCTACT	CCATCCTGAA	AGCCAAGAAC	GCAGGGATGT	CGCTGGGGGC											3046				
CAAGGGCGCC	GCCGGCCCTC	TGCCCTCCGA	GGCCGTGCAG	TGGCTGTGCC	ACCAAGCATT											3106				
CCTGCTCAAG	CTGACTCGAC	ACCGTGTAC	CTACGTGCCA	CTCCTGGGGT	CACTCAGGAC											3166				
AGCCCAGACG	CAGCTGAGTC	GGAAGCTCCC	GGGGACGACG	CTGACTGCCC	TGGAGGCCGC											3226				
AGCCAACCCG	GCACTGCCCT	CAGACTTCAA	GACCATCCTG	GACTGATGGC	CACCCGCCCA											3286				
CAGCCAGGCC	GAGAGCAGAC	ACCAGCAGCC	CTGTACGCC	GGGCTCTACG	TCCCAGGGAG											3346				
GGAGGGGCGG	CCCACACCCA	GGCCCGCACC	GCTGGGAGTC	TGAGGCCTGA	GTGAGTGTTT											3406				
GGCCGAGGCC	TGCATGTCCG	GCTGAAGGCT	GAGTGTCGGG	CTGAGGCCTG	AGCGAGTGTC											3466				
CAGCCAAGGG	CTGAGTGTC	AGCACACCTG	CCGTCTTCAC	TTCCCCACAG	GCTGGCGCTC											3526				
GGCTCCACCC	CAGGGCCAGC	TTTTCCCTCAC	CAGGAGCCCCG	GCTTCCACTC	CCCACATAGG											3586				
AATAGTCCAT	CCCCAGATTC	GCCATTGTTC	ACCCCTCGCC	CTGCCCTCCT	TTGCCCTTCCA											3646				
CCCCCACCAT	CCAGGTGGAG	ACCCTGAGAA	GGACCCTGGG	AGCTCTGGGA	ATTTGGAGTG											3706				

ACCAAAGGTG TGCCCTGTAC ACAGGCGAGG ACCCTGCACC TGGATGGGGG TCCCTGTGGG	3766
TCAAATTGGG GGGAGGTGCT GTGGGAGTAA AATACTGAAT ATATGAGTTT TTCAGTTTTG	3826
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3855

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	1	5	10	15
His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	20	25	30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	65	70	75	80
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	85	90	95	
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	100	105	110	
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	115	120	125	
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	130	135	140	
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	145	150	155	160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	165	170	175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	180	185	190	
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	195	200	205	
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	210	215	220	
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	225	230	235	240

Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp
				245					250					255	
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val
			260					265					270		
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala
		275					280					285			
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His
	290					295					300				
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro
305					310					315					320
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly
				325					330					335	
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro
			340					345					350		
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser
		355					360					365			
Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln
	370					375					380				
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His
385					390					395					400
Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg
				405					410					415	
Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln
			420					425					430		
Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu
		435					440					445			
Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe
	450					455					460				
Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser
465					470					475					480
Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser
				485					490					495	
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met
			500					505					510		
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys
		515					520					525			
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe
	530					535					540				
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe
545					550					555					560
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr
				565					570					575	

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
 755 760 765
 Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
 770 775 780
 Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg
 785 790 795 800
 Ala Ala Pro Ala Phe Gly Gly
 805

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATCGATTGGG CCCGAGATCT CGCGCGCGAG GCCTGCCATG GGACCCACTG CAGGGGCAGC

60

TGGGANGCTG	CAGGCTTCAG	GTCCCAGTGG	GGTTGCCATC	TGCCAGTAGA	AACCTGATGT	120
AGAATCAGGG	CGCGAGTGTG	GACACTGTCC	TGAATCTCAA	TGTCTCAGTG	TGTGCTGAAA	180
CATGTAGAAA	TTAAAGTCCA	TCCCTCCTAC	TCTACTGGGA	TTGAGCCCCT	TCCCTATCCC	240
CCCCCAGGGG	CAGAGGAGTT	CCTCTCACTC	CTGTGGAGGA	AGGAATGATA	CTTTGTTATT	300
TTTCACTGCT	GGTACTGAAT	CCACTGTTTC	ATTTGTTGGT	TTGTTTGT	TGTTTTGAGA	360
AGCGGTTTCA	CTCTTGTTGC	TCAGGCTGGA	NGGAGTGCAA	TGGCGCGATC	TTGGCTTACT	420
GCAGCCTCTG	CCTCCCAGGT	TCAAGTGATT	CTCCTGCTTC	CGCCTCCCAT	TTGGCTGGGA	480
TTACAGGCAC	CCGCCACCAT	GCCCAGCTAA	TTTTTTGTAT	TTTTAGTANA	NACNGGGGTG	540
GGGGTGGGGT	TCACATGTTG	GCCAAGCTGG	TCTCGAACTT	CTGAACTCAG	ATGATCCANC	600
TGCCTCTGCC	TCCTAAAATT	GCTGGGATTA	CAGGTGTNAN	CCACCATGCC	CAACTCAAAA	660
TTTACTCTGT	TTANAAACAT	CTGGGTCTAA	GGTAGGAANC	TCACCCCACT	CAATTTTTGT	720
GGTGTTTTTA	AGCCAATNAN	AAAATTTTTT	NATGTTGTTT	NNNNNNNNNN	NNNNNNNNNN	780
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	840
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	900
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	960
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	1020
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	1080
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	1140
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	1200
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	1260
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	1320
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	1380
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNCCGG	TGNNNGAGGG	1440
NGCCANGRAG	GGGGCCAGGT	TCCAANTTCC	CAACCKTTTT	WGGARGGACN	GCCCCCAGGG	1500
GGGGATRAAC	AGANTNGGGG	GKGGTWGGGT	TNAKGGTGGG	AACNCCTTNG	CSGCCTGGAG	1560
AACGTGCAAA	GAGGAAATGA	AGGGCCTGKG	TCAAGGAGCC	CAAGTNGGCG	GGGRAGTTTG	1620
CAGGGAGGCA	CTCCGGGGAG	GTCCSGCGTG	CCCGTCCAAG	GGAGCAATGC	GTCCTTCGGG	1680
TTCGTCCCCA	WGCGCGTCT	ACGCGCCTYC	CGTCCTCCCC	TTCACGTTC	GGCATTCTGT	1740
GTGCCCCGAG	CCCACGCCC	CGCGTCCGGA	CCTGGAGGCA	GCCCTGGGTC	TCCGGATCAG	1800
GCCAGCGGCC	AAAGGGTCGC	CGCACGCACC	TGTTCCCAGG	GCCTCCACAT	CATGGCCCCCT	1860
CCCTCGGGTT	ACCCACAGC	CTAGGCCGGA	TTCGACCTCT	CTCCGCTGGG	GCCCTCGCCT	1920

GGCGTCCCTG	CACCCTGGGA	GCGCGAGCGG	CGCGCGGGCG	GGGAAGCGCG	GCCCATACCC	1980
CCGGGTCCGC	CCGAAGCAG	CTGCGCTGTC	GGGGCCAGGC	CGGGCTCCCA	GTGGATTTCG	2040
GGGCACAGAC	GCCCAGGACC	GCGCTTCCCA	CGTGGCGGAA	GGACTGGGGA	CCCGGGCACC	2100
CGTCCTGCCC	CTTCACCTTC	CAGCTCCGCT	TCTTCCGCGC	GGACCCGGCC	CCGTCCCGAA	2160
CCCTTCCCAG	GTCCCGGCCC	AGCCCCCTTC	GGGCCCTCCC	AGCCCCCTCC	CTTCCTTTTC	2220
CGCGGCCCCG	CCCTCTCCTT	CGCGGCGCGA	GTTTCAGGCA	GCGCTGCGTC	CTGCTGCGCA	2280
CGTGGGAAGC	CCTGGCCCCG	GCCACCCCCG	CGATGCCGCG	CGCTCCCCGC	TGCCGAGCCG	2340
TGCGCTCCCT	GCTGCGCAGC	CACTACCGCG	AGGTGCTGCC	GCTGGCCACG	TTCGTGCGGC	2400
GCCTGGGGCC	CCAGGGCTGG	CGGCTGGTGC	AGCGCGGGGA	CCCGGCGGCT	TTCCGCGCGC	2460
TGGTGGCCCA	GTGCTGGTG	TGCGTGCCCT	GGGACGCACG	GCCGCCCCCC	GCCGCCCCCT	2520
CCTTCCGCCA	GGTGGGCCTC	CCCGGGGTGC	GCGTCCGGCT	GGGGTTGAGG	GCGGCCGGGG	2580
GGAACCAGCG	ACATGCGGAG	AGCAGCGCAG	GCGACTCAGG	GCGCTTCCCC	CGCAGGTGTC	2640
CTGCCTGAAG	GAGCTGGTGG	CCCGAGTGCT	GCAGAGGCTG	TGCGAGCGCG	GCGCGAAGAA	2700
CGTGCTGGCC	TTGGGCTTCG	CGCTGCTGGA	CGGGGCCCCG	GGGGGCCCCC	CCGAGGCCTT	2760
CACCACCAGC	GTGCGCAGCT	ACCTGCCCAA	CACGGTGACC	GACGCACTGC	GGGGGAGCGG	2820
GGCGTGGGGG	CTGCTGCTGC	GCCGCGTGGG	CGACGACGTG	CTGGTTCACC	TGCTGGCACG	2880
CTGCGCGCTC	TTTGCTGCTG	TGGCTCCCAG	CTGCGCCTAC	CAGGTGTGCG	GGCCGCCGCT	2940
GTACCAGCTC	GGCGCTGCCA	CTCAGGCCCC	GCCCCCGCCA	CACGCTAGTG	GACCCCGAAG	3000
GCCTCTGGGA	TGCGAACGGG	CCTGGAACCA	TAGCGTCAGG	GAGGCCGGGG	TCCCCCTGGG	3060
CCTGCCAGCC	CCGGGTGCCA	GGAGGCGCGG	GGGCAGTGCC	AGCCGAAGTC	TGCCGTTGCC	3120
CAAGAGGCCC	AGGCGTGGCG	CTGCCCCCTG	GCCGGAGCGG	ACGCCCCGTT	GGCAGGGGTC	3180
CTGGGCCCCA	CCGGGCAGGA	CGCGTGGAAC	GAGTGACCGT	GGTTTCTGTG	TGGTGTACAC	3240
TGCCAGACCC	GCCGAAGAAG	CCACCTCTTT	GGAGGGTGCG	CTCTCTGGCA	CGCGCCACTC	3300
CCACCCATCC	GTGGGCGGCC	AGCACCACGC	GGGCCCCCCA	TCCACATCGC	GGCCACCACG	3360
TCCCTGGGAC	ACGCCTTGTC	CCCCGGTGTA	CGCCGAGACC	AAGCACTTCC	TCTACTCCTC	3420
AGGCGACAAG	GAGCAGCTGC	GGCCCTCCTT	CCTACTCAGC	TCTCTGAGGC	CCAGCCTGAC	3480
TGGCGCTCGG	AGGCTCGTGG	AGACCATCTT	TCTGGGTTCC	AGGCCCTGGA	TGCCAGGGAC	3540
TCCCCGCAGG	TTGCCCCGCC	TGCCCGAGCG	CTACTGGCAA	ATGCGGCCCC	TGTTTCTGGA	3600
GCTGCTTGGG	AACCACGCGC	AGTGCCCCCT	CGGGGTGCTC	CTCAAGACGC	ACTGCCCCGT	3660
GCGAGCTGCG	GTCACCCAG	CAGCCGGTGT	CTGTGCCCCG	GAGAAGCCCC	AGGGCTCTGT	3720
GGCGGCCCCC	GAGGAGGAGG	ACACAGACCC	CCGTCGCCTG	GTGCAGCTGC	TCCGCCAGCA	3780

CAGCAGCCCC TGGCAGGTGT ACGGCTTCGT GCGGGCCTGC CTGCGCCGGC TGGTGCCCCC	3840
AGGCCTCTGG GGCTCCAGGC ACAACGAACG CCGCTTCCTC AGGAACACCA AGAAGTTCAT	3900
CTCCCTGGGG AAGCATGCCA AGCTCTCGCT GCAGGAGCTG ACGTGGAAGA TGAGCGTGCG	3960
GGACTGCGCT TGGCTGCGCA GGAGCCCAGG TGAGGAGGTG GTGGCCGTCG AGGGCCCAGG	4020
CCCCAGAGCT GAATGCAGTA GGGGCTCAGA AAAGGGGGCA GGCAGAGCCC TGGTCCTCCT	4080
GTCTCCATCG TCACGTGGGC ACACGTGGCT TTTCGCTCAG GACGTCGAGT GGACACGGTG	4140
ATCGAGGTCTG ACTCTAGAGG ATCCCCGGGT ACCGAGCTCG AATTCGTAAT CATGGTCATA	4200

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: intron
 - (B) LOCATION: 95..198
 - (D) OTHER INFORMATION: /note= "intron 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACCCGGCG GCTTTCCGCG CGCTGGTGGC CCAGTGCCTG GTGTGCGTGC CCTGGGACGC	60
ACGGCCGCCC CCCGCCGCC CCTCCTTCCG CCAGGTGGGC CTCCCCGGGG TCGGCGTCCG	120
GCTGGGGTTG AGGGCGGCCG GGGGGAACCA GCGACATGCG GAGAGCAGCG CAGGCGACTC	180
AGGGCGCTTC CCCCGCAGGT GTCCTGCCTG AAGGAGCTGG TGGCCCGAGT GCTGCAGAGG	240

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..389
 - (D) OTHER INFORMATION: /note= "expressed sequence tag (EST) AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCAAGTTCC TGCACTGGCT GATGAGTGTG TACGTCGTG AGCTGCTCAG GTCTTTCTTT	60
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TATGTCACGG AGACCACGTT TCAAAAGAAC AGGCTCTTTT TCTACCGGAA GAGTGTCTGG 120
 AGCAAGTTGC AAAGCATTGG AATCAGACAG CACTTGAAGA GGGTGCAGCT GCGGGACGTG 180
 TCGGAAGCAG AGGTCAGGCA GCATCGGGAA GCCAGGCCCG CCCTGCTGAC GTCCAGACTC 240
 CGCTTCATCC CCAAGCCTGA CGGGCTGCGG CCGATTGTGA ACATGGACTA CGTCGTGGGA 300
 GCCAGAACGT TCCGCAGAGA AAAGAGGGCC GAGCGTCTCA CCTCGAGGGT GAAGGCACTG 360
 TTCAGCGTGC TCAACTACGA GCGGGCGCG 389

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: /note= "182 basepair sequence deleted in clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCTACCTTGA CAGACCTCCA GCCGTACATG CGACAGTTCG TGGCTCACCT GCAGGAGACC 60
 AGCCCGCTGA GGGATGCCGT CGTCATCGAG CAGAGCTCCT CCCTGAATGA GGCCAGCAGT 120
 GGCCTCTTCG ACGTCTTCCT ACGCTTCATG TGCCACCACG CCGTGCGCAT CAGGGGCAAG 180
 TC 182

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..259
- (D) OTHER INFORMATION: /note= "protein encoded by clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr

1	5	10	15
Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val	20	25	30
Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val	35	40	45
Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala	50	55	60
Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp	65	70	80
Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr	85	90	95
Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala	100	105	110
Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu	115	120	125
Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr	130	135	140
Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe	145	150	155
Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg	165	170	175
Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys	180	185	190
Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg	195	200	205
Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro Ala	210	215	220
Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg His	225	230	235
Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro Ala	245	250	255
Phe Gly Gly			

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Gln or Arg"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 28
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Trp
1				5					10					15	
	Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa
			20					25					30		
	Xaa	Trp													

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Leu or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Gln or Arg"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 30
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Phe or Tyr"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Trp
1				5					10					15	
Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa
			20					25					30		
Xaa	Xaa	Trp													
		35													

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: /note= "TRT motifs from human"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	1	5	10	15
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	20	25	30	
Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	35	40	45	
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	50	55	60	
Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	65	70	75	80
Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	85	90	95	
Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	100	105	110	
Leu	Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	115	120	125	

Ala

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile	Ser	Glu	Ile	Glu	Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe
 20 25 30
 Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe
 35 40 45
 Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe
 50 55 60
 Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met
 65 70 75 80
 Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp
 85 90 95
 Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys
 100 105
 Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile
 115 120 125
 Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
 130 135 140
 Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser
 145 150 155 160
 Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
 165 170 175
 Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
 180 185 190
 Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
 195 200 205
 Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
 210 215 220
 Lys Tyr Ala Thr Ile His Ala Thr Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu	Lys	Asp	Phe	Arg	Trp	Leu	Phe	Ile	Ser	Asp	Ile	Trp	Phe	Thr	Lys	1	5	10	15
His	Asn	Phe	Glu	Asn	Leu	Asn	Gln	Leu	Ala	Ile	Cys	Phe	Ile	Ser	Trp	20	25	30	
Leu	Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr	Cys	35	40	45	
Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp	Thr	50	55	60	
Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr	Phe	Lys	Thr	Tyr	65	70	75	80
Leu	Val	Glu	Asn	Asn	Val	Cys	Arg	Asn	His	Asn	Ser	Tyr	Thr	Leu	Ser	85	90	95	
Asn	Phe	Asn	His	Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn	100	105	110	
Glu	Phe	Arg	Ile	Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp	Glu	Glu	Glu	115	120	125	
Phe	Thr	Ile	Tyr	Lys	Glu	Asn	His	Lys	Asn	Ala	Ile	Gln	Pro	Thr	Gln	130	135	140	
Lys	Ile	Leu	Glu	Tyr	Leu	Arg	Asn	Lys	Arg	Pro	Thr	Ser	Phe	Thr	Lys	145	150	155	160
Ile	Tyr	Ser	Pro	Thr	Gln	Ile	Ala	Asp	Arg	Ile	Lys	Glu	Phe	Lys	Gln	165	170	175	
Arg	Leu	Leu	Lys	Lys	Phe	Asn	Asn	Val	Leu	Pro	Glu	Leu	Tyr	Phe	Met	180	185	190	
Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile	Pro	Arg	Met	Glu	Cys	195	200	205	
Met	Arg	Ile	Leu	Lys	Asp	Ala	Leu	Lys	Asn	Glu	Asn	Gly	Phe	Phe	Val	210	215	220	
Arg	Ser	Gln	Tyr	Phe	Phe	Asn	Thr	Asn	225	230									

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr	Arg	Glu	Ile	Ser	Trp	Met	Gln	Val	Glu	Thr	Ser	Ala	Lys	His	Phe	
1				5					10					15		
Tyr	Tyr	Phe	Asp	His	Glu	Asn	Ile	Tyr	Val	Leu	Trp	Lys	Leu	Leu	Arg	
		20					25					30				
Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr	
		35				40					45					
Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys	
	50				55					60						
Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	Ile	Ala	Asp	Leu	Lys	Lys	
65				70					75					80		
Glu	Thr	Leu	Ala	Glu	Val	Gln	Glu	Lys	Glu	Val	Glu	Glu	Trp	Lys	Lys	
			85				90						95			
Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	
		100					105						110			
Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	
	115						120					125				
Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr	Lys	Leu	Leu	Asn	Ser	His	
	130				135						140					
Leu	Met	Leu	Lys	Thr	Leu	Lys	Asn	Arg	Met	Phe	Lys	Asp	Pro	Phe	Gly	
145				150						155					160	
Phe	Ala	Val	Phe	Asn	Tyr	Asp	Asp	Val	Met	Lys	Lys	Tyr	Glu	Glu	Phe	
			165					170					175			
Val	Cys	Lys	Trp	Lys	Gln	Val	Gly	Gln	Pro	Lys	Leu	Phe	Phe	Ala	Thr	
			180				185						190			
Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	
	195						200					205				
Thr	Phe	Leu	Lys	Thr	Thr	Lys	Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	
	210				215						220					
Thr	Ala	Gln	Ile	Leu	Lys	Arg	Lys	Asn								
225					230											

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide

- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif T"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly, Ser, Thr, Tyr, Cys, Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Xaa Phe Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Xaa Arg Xaa Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif 2"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Phe Arg Xaa Ile
1

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif A"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = charged amino acid, Asp, Glu, His, Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro Xaa Leu Tyr Phe Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif B'"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ile Pro Gln Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Leu Arg Leu
1

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..7
 (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
 from motif C"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 Ala, Leu, Ile, Val, Pro, Phe, Trp
 or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asp Asp Phe Leu Xaa Ile Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..48
 (D) OTHER INFORMATION: /note= "motif T peptide from
 Schizosaccharomyces pombe TRT tezl"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
 1 5 10 15
 Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
 20 25 30
 Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met
 35 40 45

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Schizosaccharomyces pombe TRT tezip"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr Leu Pro Pro Ala Val
1 5 10 15

Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu
20 25 30

Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn Lys Lys Met Leu Val
35 40 45

Ser Thr Asn Gln Thr Leu
50

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..34

(D) OTHER INFORMATION: /note= "motif A peptide from
Schizosaccharomyces pombe TRT tezip"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr
1 5 10 15

Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys Lys Leu
20 25 30

Lys Asp

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from Schizosaccharomyces pombe TRT tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser
1 5 10 15

Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu
20 25 30

Ser Phe Thr
35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from Schizosaccharomyces pombe TRT tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
1 5 10 15

Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
20 25 30

Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile
35 40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11

(D) OTHER INFORMATION: /note= "motif E peptide from
Schizosaccharomyces pombe TRT tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "motif T peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr
1 5 10 15
Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
20 25 30
Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
1 5 10 15

Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
20 25 30
Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
35 40 45
Arg Leu Thr Ser Arg Val
50

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..34
 - (D) OTHER INFORMATION: /note= "motif A peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
1 5 10 15
Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
20 25 30
Lys Pro

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..35
 - (D) OTHER INFORMATION: /note= "motif B' peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser
1 5 10 15
Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe
20 25 30

Ala Gly Ile
35

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
1				5					10					15	
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
			20					25					30		
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val					
			35				40								

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..48
(D) OTHER INFORMATION: /note= "motif T peptide from Euplotes
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr
1				5					10					15	
Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys
			20					25					30		
Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	Ile	Ala	Asp	Leu	Lys	Lys
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..54
(D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Lys	Glu	Val	Glu	Glu	Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys
1				5					10					15	
Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe
			20				25					30			
Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr
		35				40					45				
Asn	Thr	Lys	Leu	Leu	Asn										
		50													

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..34
(D) OTHER INFORMATION: /note= "motif A peptide from Euplotes
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
1 5 10 15
Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
20 25 30
Leu Leu

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /note= "motif B' peptide from Euplotes
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser
1 5 10 15
Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu
20 25 30
Gly Phe Leu
35

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	Ile	Thr	Thr	Gln	Glu	Asn
1				5					10					15	
Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	Asn	Val	Ser	Arg	Glu	Asn
		20						25					30		
Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr					
		35					40								

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	Ile	Ser	Ile
1				5				10		

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: /note= "motif T peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1 5 10 15
Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
20 25 30
Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /note= "motif 1 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn Phe Asn His Ser Lys
1 5 10 15
Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
20 25

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..29
(D) OTHER INFORMATION: /note= "motif 2 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
1 5 10 15

Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..34
 (D) OTHER INFORMATION: /note= "motif A peptide from
 Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
 1 5 10 15
 Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
 20 25 30
 Lys Asn

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..35
 (D) OTHER INFORMATION: /note= "motif B' peptide from
 Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser
 1 5 10 15
 Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser
 20 25 30
 Glu Phe Lys
 35

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..43
(D) OTHER INFORMATION: /note= "motif C and D peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1           5           10           15
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
          20           25           30
Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
          35           40
```

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /note= "motif E peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
Lys Glu Leu Glu Val Trp Lys His Ser Ser Thr
1           5           10
```

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus non-telomerase RT sequence from motif B'"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Xaa Pro Gln Gly
1

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "consensus non-telomerase RT sequence from motif C"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,

Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Asp Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..55
(D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Leu Ser Asn Glu Leu Gly Thr Gly Lys Phe Lys Phe Lys Pro Met Arg
1 5 10 15
Ile Val Asn Ile Pro Lys Pro Lys Gly Gly Ile Arg Pro Leu Ser Val
20 25 30
Gly Asn Pro Arg Asp Lys Ile Val Gln Glu Val Met Arg Met Ile Leu
35 40 45
Asp Thr Ile Phe Asp Lys Lys
50 55

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 1..34
(D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded

mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Phe Gly Gly Ser Asn Trp Phe Ile Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15
Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
 20 25 30
Ser Asp

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Thr Tyr His Lys Pro Met Leu Gly Leu Pro Gln Gly Ser Leu Ile Ser
1 5 10 15
Pro Ile Leu Cys Asn Ile Val Met Thr Leu Val Asp Asn Trp Leu Glu
 20 25 30
Asp Tyr Ile
 35

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "motif C peptide from
Saccharomyces cerevisiae cytochrome

oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15

Asn

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif D peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys Met Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
1 5 10 15

Thr Ile Asn Glu Lys Thr Leu Ile
20 25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Glu Thr Pro Ala Arg Phe Leu Gly Tyr Asn Ile
 1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
 Drosophila melanogaster TART non-LTR
 retrotransposable element reverse
 transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ser Ile Leu Arg Ile Gly Tyr Tyr Pro Asp Ala Trp Lys His Ala Gln
 1 5 10 15

Val Lys Met Ile Leu Lys Pro Gly Lys Ser
 20 25

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "motif 2 peptide from
 Drosophila melanogaster TART non-LTR
 retrotransposable element reverse
 transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Arg Pro Ile Ser Leu Leu Ser Gly Leu Ser Lys Met Phe Glu Arg
 1 5 10 15

Leu Leu Leu Lys Arg Leu Phe Arg Val Asp Leu Phe Lys
 20 25

(D) OTHER INFORMATION: /note= "motif 2 and A peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp
1				5					10					15	
Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys
			20					25					30		
Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val
		35					40					45			
Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
(B) LOCATION: 35
(D) OTHER INFORMATION: /note= "motif B' peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser
1				5					10					15	
Pro	Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Lys
			20					25					30		
Lys	Gln	Asn													
		35													

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..17
(D) OTHER INFORMATION: /note= "motif C peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..37
(D) OTHER INFORMATION: /note= "motif D and E peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
1 5 10 15

Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
20 25 30

Met Gly Ile Thr Leu
35

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..4
(D) OTHER INFORMATION: /note= "consensus telomerase RT finger sequence from motif 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ile Pro Lys Lys

1

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "consensus telomerase RT palm,
primer grip sequence from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Leu Leu Arg Leu
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT palm,
primer grip sequence from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Phe Leu
1

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "telomerase specific motif T peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr
1 5 10 15
Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
 20 25 30
Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T' peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Glu Ala Glu Val Arg
1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif 1 and 2 peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B' peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu
 1 5 10 15
 Leu Cys Ser Leu Cys Tyr
 20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif D peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "telomerase specific motif T peptide from Schizosaccharomyces pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
1 5 10 15
Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
20 25 30
Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile
35 40

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T' peptide from Schizosaccharomyces pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Glu Asn Asn Val Arg
1 5

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /note= "telomerase RT finger motif
1 and 2 peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Arg	Lys	Lys	Tyr	Phe	Val	Arg	Ile	Asp	Ile	Lys	Ser	Cys	Tyr	Asp	Arg
1				5					10					15	

Ile

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B'
peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
 1 5 10 15
 Leu Cys His Phe Tyr Met
 20

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..13
 - (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip
motif C peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip
motif D peptide from Schizosaccharomyces
pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from Schizosaccharomyces pombe TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "telomerase specific motif T peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 1 5 10 15

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 20 25 30

Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'
peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Glu Lys Glu Val Glu
1 5

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif
1 and 2 peptide from Euplotes
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Phe Arg Pro Ile Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
1 5 10 15
Val

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B'
peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
1 5 10 15
Leu Ser Ser Phe Tyr Tyr
20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip
motif C peptide from Euplotes
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..16
(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif D peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Trp	Ile	Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..42

(D) OTHER INFORMATION: /note= "telomerase specific motif T
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Trp	Leu	Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr
1				5					10					15	
Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp
		20						25					30		
Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile						
		35					40								

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Glu	Asn	Asn	Val	Cys
1				5

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif 1
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..5
(D) OTHER INFORMATION: /note= "telomerase RT finger motif 2
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe Arg Ile Ile Ala
1 5

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /note= "telomerase RT finger motif A
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser
1 5 10 15
Ile

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B'
peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser	Ala	Pro
1				5					10					15	
Ile Val Asp Leu Val Tyr															
20															

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip
motif C peptide from Saccharomyces
cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu	Ile	Leu	Lys	Leu	Ala	Asp	Asp	Phe	Leu	Ile	Ile	Ser
1				5					10			

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip

motif D peptide from *Saccharomyces cerevisiae* EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from *Saccharomyces cerevisiae* EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp Lys His Ser Ser Thr Met Asn Asn Phe His
1 5 10

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /note= "NFkappaB CS1 binding site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGGRHTYYHC

10

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "NFkappaB MHC I.2 binding site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGGGCTTCCC C

11

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "NFkappaB CS2 binding site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

RGGGRMTYYC C

11

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein_bind
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "topoisomerase II cleavage site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

RNYNNCNGY NGKTINYNY

18

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 101..3196
- (D) OTHER INFORMATION: /note= "Euplotes aediculatus 123 kDa telomerase protein subunit (TRT)"
/codon= (seq: "tga", aa: Cys)
/product= "Euplotes aediculatus 123 kDa telomerase protein subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAAACCCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
TTAATAAGCT CAGATTTTAA ATATTAATTA CAAACCTAA ATG GAG GTT GAT GTT	115
Met Glu Val Asp Val	5
1	
GAT AAT CAA GCT GAT AAT CAT GGC ATT CAC TCA GCT CTT AAG ACT TGT	163
Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala Leu Lys Thr Cys	20
10	15
GAA GAA ATT AAA GAA GCT AAA ACG TTG TAC TCT TGG ATC CAG AAA GTT	211
Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp Ile Gln Lys Val	35
25	30
ATT AGA TGA AGA AAT CAA TCT CAA AGT CAT TAT AAA GAT TTA GAA GAT	259
Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys Asp Leu Glu Asp	50
40	45
ATT AAA ATA TTT GCG CAG ACA AAT ATT GTT GCT ACT CCA CGA GAC TAT	307
Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr Pro Arg Asp Tyr	65
55	60
AAT GAA GAA GAT TTT AAA GTT ATT GCA AGA AAA GAA GTA TTT TCA ACT	355
Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu Val Phe Ser Thr	85
70	75
GGA CTA ATG ATC GAA CTT ATT GAC AAA TGC TTA GTT GAA CTT CTT TCA	403
Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val Glu Leu Leu Ser	100
90	95
TCA AGC GAT GTT TCA GAT AGA CAA AAA CTT CAA TGA TTT GGA TTT CAA	451
Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys Phe Gly Phe Gln	115
105	110
CTT AAG GGA AAT CAA TTA GCA AAG ACC CAT TTA TTA ACA GCT CTT TCA	499
Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu Thr Ala Leu Ser	130
120	125
ACT CAA AAG CAG TAT TTC TTT CAA GAC GAA TGG AAC CAA GTT AGA GCA	547

Thr	Gln	Lys	Gln	Tyr	Phe	Phe	Gln	Asp	Glu	Trp	Asn	Gln	Val	Arg	Ala	
135						140					145					
ATG	ATT	GGA	AAT	GAG	CTC	TTC	CGA	CAT	CTC	TAC	ACT	AAA	TAT	TTA	ATA	595
Met	Ile	Gly	Asn	Glu	Leu	Phe	Arg	His	Leu	Tyr	Thr	Lys	Tyr	Leu	Ile	
150					155					160					165	
TTC	CAG	CGA	ACT	TCT	GAA	GGA	ACT	CTT	GTT	CAA	TTT	TGC	GGG	AAT	AAC	643
Phe	Gln	Arg	Thr	Ser	Glu	Gly	Thr	Leu	Val	Gln	Phe	Cys	Gly	Asn	Asn	
				170					175					180		
GTT	TTT	GAT	CAT	TTG	AAA	GTC	AAC	GAT	AAG	TTT	GAC	AAA	AAG	CAA	AAA	691
Val	Phe	Asp	His	Leu	Lys	Val	Asn	Asp	Lys	Phe	Asp	Lys	Lys	Gln	Lys	
			185					190					195			
GGT	GGA	GCA	GCA	GAC	ATG	AAT	GAA	CCT	CGA	TGT	TGA	TCA	ACC	TGC	AAA	739
Gly	Gly	Ala	Ala	Asp	Met	Asn	Glu	Pro	Arg	Cys	Cys	Ser	Thr	Cys	Lys	
		200					205					210				
TAC	AAT	GTC	AAG	AAT	GAG	AAA	GAT	CAC	TTT	CTC	AAC	AAC	ATC	AAC	GTG	787
Tyr	Asn	Val	Lys	Asn	Glu	Lys	Asp	His	Phe	Leu	Asn	Asn	Ile	Asn	Val	
	215					220					225					
CCG	AAT	TGG	AAT	AAT	ATG	AAA	TCA	AGA	ACC	AGA	ATA	TTT	TAT	TGC	ACT	835
Pro	Asn	Trp	Asn	Asn	Met	Lys	Ser	Arg	Thr	Arg	Ile	Phe	Tyr	Cys	Thr	
230					235					240					245	
CAT	TTT	AAT	AGA	AAT	AAC	CAA	TTC	TTC	AAA	AAG	CAT	GAG	TTT	GTG	AGT	883
His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys	His	Glu	Phe	Val	Ser	
				250					255					260		
AAC	AAA	AAC	AAT	ATT	TCA	GCG	ATG	GAC	AGA	GCT	CAG	ACG	ATA	TTC	ACG	931
Asn	Lys	Asn	Asn	Ile	Ser	Ala	Met	Asp	Arg	Ala	Gln	Thr	Ile	Phe	Thr	
			265					270					275			
AAT	ATA	TTC	AGA	TTT	AAT	AGA	ATT	AGA	AAG	AAG	CTA	AAA	GAT	AAG	GTT	979
Asn	Ile	Phe	Arg	Phe	Asn	Arg	Ile	Arg	Lys	Lys	Leu	Lys	Asp	Lys	Val	
		280					285					290				
ATC	GAA	AAA	ATT	GCC	TAC	ATG	CTT	GAG	AAA	GTC	AAA	GAT	TTT	AAC	TTC	1027
Ile	Glu	Lys	Ile	Ala	Tyr	Met	Leu	Glu	Lys	Val	Lys	Asp	Phe	Asn	Phe	
	295					300					305					
AAC	TAC	TAT	TTA	ACA	AAA	TCT	TGT	CCT	CTT	CCA	GAA	AAT	TGG	CGG	GAA	1075
Asn	Tyr	Tyr	Leu	Thr	Lys	Ser	Cys	Pro	Leu	Pro	Glu	Asn	Trp	Arg	Glu	
310					315					320					325	
CGG	AAA	CAA	AAA	ATC	GAA	AAC	TTG	ATA	AAT	AAA	ACT	AGA	GAA	GAA	AAG	1123
Arg	Lys	Gln	Lys	Ile	Glu	Asn	Leu	Ile	Asn	Lys	Thr	Arg	Glu	Glu	Lys	
				330					335					340		
TCG	AAG	TAC	TAT	GAA	GAG	CTG	TTT	AGC	TAC	ACA	ACT	GAT	AAT	AAA	TGC	1171
Ser	Lys	Tyr	Tyr	Glu	Glu	Leu	Phe	Ser	Tyr	Thr	Thr	Asp	Asn	Lys	Cys	
			345					350					355			
GTC	ACA	CAA	TTT	ATT	AAT	GAA	TTT	TTC	TAC	AAT	ATA	CTC	CCC	AAA	GAC	1219
Val	Thr	Gln	Phe	Ile	Asn	Glu	Phe	Phe	Tyr	Asn	Ile	Leu	Pro	Lys	Asp	
		360					365					370				
TTT	TTG	ACT	GGA	AGA	AAC	CGT	AAG	AAT	TTT	CAA	AAG	AAA	GTT	AAG	AAA	1267
Phe	Leu	Thr	Gly	Arg	Asn	Arg	Lys	Asn	Phe	Gln	Lys	Lys	Val	Lys	Lys	
	375					380					385					

TAT GTG GAA CTA AAC AAG CAT GAA CTC ATT CAC AAA AAC TTA TTG CTT Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu Leu Leu 390 395 400 405	1315
GAG AAG ATC AAT ACA AGA GAA ATA TCA TGG ATG CAG GTT GAG ACC TCT Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser 410 415 420	1363
GCA AAG CAT TTT TAT TAT TTT GAT CAC GAA AAC ATC TAC GTC TTA TGG Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp 425 430 435	1411
AAA TTG CTC CGA TGG ATA TTC GAG GAT CTC GTC GTC TCG CTG ATT AGA Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg 440 445 450	1459
TGA TTT TTC TAT GTC ACC GAG CAA CAG AAA AGT TAC TCC AAA ACC TAT Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr 455 460 465	1507
TAC TAC AGA AAG AAT ATT TGG GAC GTC ATT ATG AAA ATG TCA ATC GCA Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala 470 475 480 485	1555
GAC TTA AAG AAG GAA ACG CTT GCT GAG GTC CAA GAA AAA GAG GTT GAA Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu 490 495 500	1603
GAA TGG AAA AAG TCG CTT GGA TTT GCA CCT GGA AAA CTC AGA CTA ATA Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile 505 510 515	1651
CCG AAG AAA ACT ACT TTC CGT CCA ATT ATG ACT TTC AAT AAG AAG ATT Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile 520 525 530	1699
GTA AAT TCA GAC CGG AAG ACT ACA AAA TTA ACT ACA AAT ACG AAG TTA Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu 535 540 545	1747
TTG AAC TCT CAC TTA ATG CTT AAG ACA TTG AAG AAT AGA ATG TTT AAA Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys 550 555 560 565	1795
GAT CCT TTT GGA TTC GCT GTT TTT AAC TAT GAT GAT GTA ATG AAA AAG Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys 570 575 580	1843
TAT GAG GAG TTT GTT TGC AAA TGG AAG CAA GTT GGA CAA CCA AAA CTC Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu 585 590 595	1891
TTC TTT GCA ACT ATG GAT ATC GAA AAG TGA TAT GAT AGT GTA AAC AGA Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg 600 605 610	1939
GAA AAA CTA TCA ACA TTC CTA AAA ACT ACT AAA TTA CTT TCT TCA GAT Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp 615 620 625	1987
TTC TGG ATT ATG ACT GCA CAA ATT CTA AAG AGA AAG AAT AAC ATA GTT Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn Ile Val 630 635 640 645	2035

630		635		640		645	
ATC GAT TCG AAA AAC TTT AGA AAG AAA GAA ATG AAA GAT TAT TTT AGA							2083
Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr Phe Arg							
	650			655		660	
CAG AAA TTC CAG AAG ATT GCA CTT GAA GGA GGA CAA TAT CCA ACC TTA							2131
Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro Thr Leu							
	665			670		675	
TTC AGT GTT CTT GAA AAT GAA CAA AAT GAC TTA AAT GCA AAG AAA ACA							2179
Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys Lys Thr							
	680			685		690	
TTA ATT GTT GAA GCA AAG CAA AGA AAT TAT TTT AAG AAA GAT AAC TTA							2227
Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp Asn Leu							
	695			700		705	
CTT CAA CCA GTC ATT AAT ATT TGC CAA TAT AAT TAC ATT AAC TTT AAT							2275
Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn Phe Asn							
	710			715		720	725
GGG AAG TTT TAT AAA CAA ACA AAA GGA ATT CCT CAA GGT CTT TGA GTT							2323
Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val							
	730			735		740	
TCA TCA ATT TTG TCA TCA TTT TAT TAT GCA ACA TTA GAG GAA AGC TCC							2371
Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser							
	745			750		755	
TTA GGA TTC CTT AGA GAT GAA TCA ATG AAC CCT GAA AAT CCA AAT GTT							2419
Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro Asn Val							
	760			765		770	
AAT CTT CTA ATG AGA CTT ACA GAT GAC TAT CTT TTG ATT ACA ACT CAA							2467
Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln							
	775			780		785	
GAG AAT AAT GCA GTA TTG TTT ATT GAG AAA CTT ATA AAC GTA AGT CGT							2515
Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg							
	790			795		800	805
GAA AAT GGA TTT AAA TTC AAT ATG AAG AAA CTA CAG ACT AGT TTT CCA							2563
Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro							
	810			815		820	
TTA AGT CCA AGC AAA TTT GCA AAA TAC GGA ATG GAT AGT GTT GAG GAG							2611
Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val Glu Glu							
	825			830		835	
CAA AAT ATT GTT CAA GAT TAC TGC GAT TGG ATT GGC ATC TCA ATT GAT							2659
Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile Asp							
	840			845		850	
ATG AAA ACT CTT GCT TTA ATG CCA AAT ATT AAC TTG AGA ATA GAA GGA							2707
Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile Glu Gly							
	855			860		865	
ATT CTG TGT ACA CTC AAT CTA AAC ATG CAA ACA AAG AAA GCA TCA ATG							2755
Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala Ser Met							
	870			875		880	885

TGG CTC AAG AAG AAA CTA AAG TCG TTT TTA ATG AAT AAC ATT ACC CAT	2803
Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile Thr His	
890 895 900	
TAT TTT AGA AAG ACG ATT ACA ACC GAA GAC TTT GCG AAT AAA ACT CTC	2851
Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys Thr Leu	
905 910 915	
AAC AAG TTA TTT ATA TCA GGC GGT TAC AAA TAC ATG CAA TGA GCC AAA	2899
Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys Ala Lys	
920 925 930	
GAA TAC AAG GAC CAC TTT AAG AAG AAC TTA GCT ATG AGC AGT ATG ATC	2947
Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser Met Ile	
935 940 945	
GAC TTA GAG GTA TCT AAA ATT ATA TAC TCT GTA ACC AGA GCA TTC TTT	2995
Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala Phe Phe	
950 955 960 965	
AAA TAC CTT GTG TGC AAT ATT AAG GAT ACA ATT TTT GGA GAG GAG CAT	3043
Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu Glu His	
970 975 980	
TAT CCA GAC TTT TTC CTT AGC ACA CTG AAG CAC TTT ATT GAA ATA TTC	3091
Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu Ile Phe	
985 990 995	
AGC ACA AAA AAG TAC ATT TTC AAC AGA GTT TGC ATG ATC CTC AAG GCA	3139
Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu Lys Ala	
1000 1005 1010	
AAA GAA GCA AAG CTA AAA AGT GAC CAA TGT CAA TCT CTA ATT CAA TAT	3187
Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile Gln Tyr	
1015 1020 1025	
GAT GCA TAGTCGACTA TTCTAACTTA TTTTGGAAG TTAATTTTCA ATTTTGTCT	3243
Asp Ala	
1030	
TATATACTGG GGTTTTGGGG TTTTGGGGTT TTGGGG	3279

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met	Glu	Val	Asp	Val	Asp	Asn	Gln	Ala	Asp	Asn	His	Gly	Ile	His	Ser
1				5					10					15	
Ala	Leu	Lys	Thr	Cys	Glu	Glu	Ile	Lys	Glu	Ala	Lys	Thr	Leu	Tyr	Ser
			20					25					30		
Trp	Ile	Gln	Lys	Val	Ile	Arg	Cys	Arg	Asn	Gln	Ser	Gln	Ser	His	Tyr
	35						40					45			

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
 50 55 60
 Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
 65 70 75 80
 Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
 85 90 95
 Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
 100 105 110
 Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
 115 120 125
 Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
 130 135 140
 Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
 145 150 155 160
 Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
 165 170 175
 Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
 180 185 190
 Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
 195 200 205
 Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
 210 215 220
 Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
 225 230 235 240
 Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
 245 250 255
 His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
 260 265 270
 Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
 275 280 285
 Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
 290 295 300
 Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
 305 310 315 320
 Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
 325 330 335
 Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
 340 345 350
 Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
 355 360 365
 Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
 370 375 380

Lys	Lys	Val	Lys	Lys	Tyr	Val	Glu	Leu	Asn	Lys	His	Glu	Leu	Ile	His
385					390					395					400
Lys	Asn	Leu	Leu	Leu	Glu	Lys	Ile	Asn	Thr	Arg	Glu	Ile	Ser	Trp	Met
			405						410					415	
Gln	Val	Glu	Thr	Ser	Ala	Lys	His	Phe	Tyr	Tyr	Phe	Asp	His	Glu	Asn
			420					425					430		
Ile	Tyr	Val	Leu	Trp	Lys	Leu	Leu	Arg	Trp	Ile	Phe	Glu	Asp	Leu	Val
		435					440					445			
Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser
	450					455					460				
Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met
465					470					475					480
Lys	Met	Ser	Ile	Ala	Asp	Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln
				485					490						495
Glu	Lys	Glu	Val	Glu	Glu	Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly
			500					505					510		
Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr
		515					520					525			
Phe	Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr
	530					535					540				
Thr	Asn	Thr	Lys	Leu	Leu	Asn	Ser	His	Leu	Met	Leu	Lys	Thr	Leu	Lys
545					550					555					560
Asn	Arg	Met	Phe	Lys	Asp	Pro	Phe	Gly	Phe	Ala	Val	Phe	Asn	Tyr	Asp
				565					570					575	
Asp	Val	Met	Lys	Lys	Tyr	Glu	Glu	Phe	Val	Cys	Lys	Trp	Lys	Gln	Val
			580					585						590	
Gly	Gln	Pro	Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr
		595					600					605			
Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys
	610					615					620				
Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	Thr	Ala	Gln	Ile	Leu	Lys	Arg
625					630					635					640
Lys	Asn	Asn	Ile	Val	Ile	Asp	Ser	Lys	Asn	Phe	Arg	Lys	Lys	Glu	Met
				645					650					655	
Lys	Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly
			660					665					670		
Gln	Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu
		675					680					685			
Asn	Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe
	690					695					700				
Lys	Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn
705					710					715					720

Tyr	Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	725	730	735
Gln	Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	740	745	750
Leu	Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro	755	760	765
Glu	Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	770	775	780
Leu	Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	785	790	795
Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	805	810	815
Gln	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met	820	825	830
Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile	835	840	845
Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn	850	855	860
Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr	865	870	875
Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met	885	890	895
Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe	900	905	910
Ala	Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr	915	920	925
Met	Gln	Cys	Ala	Lys	Glu	Tyr	Lys	Asp	His	Phe	Lys	Lys	Asn	Leu	Ala	930	935	940
Met	Ser	Ser	Met	Ile	Asp	Leu	Glu	Val	Ser	Lys	Ile	Ile	Tyr	Ser	Val	945	950	955
Thr	Arg	Ala	Phe	Phe	Lys	Tyr	Leu	Val	Cys	Asn	Ile	Lys	Asp	Thr	Ile	965	970	975
Phe	Gly	Glu	Glu	His	Tyr	Pro	Asp	Phe	Phe	Leu	Ser	Thr	Leu	Lys	His	980	985	990
Phe	Ile	Glu	Ile	Phe	Ser	Thr	Lys	Lys	Tyr	Ile	Phe	Asn	Arg	Val	Cys	995	1000	1005
Met	Ile	Leu	Lys	Ala	Lys	Glu	Ala	Lys	Leu	Lys	Ser	Asp	Gln	Cys	Gln	1010	1015	1020
Ser	Leu	Ile	Gln	Tyr	Asp	Ala										1025	1030	

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5544 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: join(959..1216, 1273..1353, 1425..1543,
 1595..1857, 1894..2286, 2326..2396, 2436..2705,
 2746..2862, 2914..3083, 3125..3309, 3356..3504,
 3546..3759, 3797..4046, 4086..4252, 4296..4392,
 4435..4597)
 (D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe
 telomerase catalytic subunit (TRT) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTTCG	240
GGTTCGCTTA CTTTAAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGAAA GTTTTTTGAT	540
GCTTGACACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTTCTA TTTTCTATT TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTCACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780
TGTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA	840
AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA	900
TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG	1006
Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu	
1 5 10 15	
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT	1054
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val	
20 25 30	

TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu 35 40 45	1102
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val 50 55 60	1150
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro 65 70 75 80	1198
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTTG ATTTTTTTCT Lys Cys Ser Gln Ser Glu 85	1246
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG Leu Ile Ala Asn Val Val Lys Gln Met 90 95	1299
TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe 100 105 110	1347
TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val 115 120	1454
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile 125 130 135	1502
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Glu Ile 140 145 150	1543
GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu 155 160 165 170	1646
GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser	1838

220	225	230	
TAT AAG AAG TTT AAG CAA G	GTA	CTA	CTGTTATCCT TCATAACTAA
Tyr Lys Lys Phe Lys Gln			
235	240		1887
TTTTAG	AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA		1934
	Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr		
	245	250	
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA			1982
Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile			
255	260	265	270
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA			2030
Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser			
	275	280	285
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT			2078
Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile			
	290	295	300
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC			2126
Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr			
	305	310	315
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT			2174
Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu			
	320	325	330
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT			2222
Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile			
	335	340	345
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT			2270
Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe			
	355	360	365
GAG ATA ATA TTA AAA G	GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC		2327
Glu Ile Ile Leu Lys			Asp
	370		
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT			2375
Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His			
	375	380	385
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT			2426
Tyr Leu Met Ser Asn Ile Lys			
	390	395	
AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA			2474
Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser			
	400	405	
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT			2522
Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe			
	410	415	420
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA			2570
Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu			
	425	430	435
			440

CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT	2618
Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr	
445 450 455	
GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT	2666
Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile	
460 465 470	
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA	2715
Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu	
475 480 485	
GTATTTTTTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG	2769
Asn Asn Val Arg Met Asp Thr Gln	
490	
AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT	2817
Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn	
495 500 505	
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG	2862
Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys	
510 515 520	
GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT	2919
Met Gly	
525	
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967
Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val	
530 535 540	
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA	3015
Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro	
545 550 555	
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT	3063
Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu	
560 565 570	
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT	3113
Leu Lys His Arg Met Phe Gly	
575 580	
TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC	3161
Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser	
585 590	
TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG	3209
Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys	
595 600 605	
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT	3257
Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His	
610 615 620 625	
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC	3305
Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser	
630 635 640	
TAT T GTAAGTTTAT TTTTTCATTG GAATTTTTTA ACAAATTCTT TTTTAG TT	3357
Tyr Phe	

GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501
AAG GTATACCAAT TGTGAATTG TAATAACACT AATGAACTA G ATA GGA AAT Lys Ile Gly Asn 695	3554
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710	3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725	3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740	3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755	3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA Leu Ser Leu Arg Gly 760	3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780	3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu 800 805 810	3942
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser 815 820 825	3990
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys 830 835 840	4038
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG Ile Leu Arg Ser 845	4089

AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser 850 855 860	4137
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys 865 870 875 880	4185
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro 885 890 895	4233
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT Gln Arg Met Phe Ile Thr 900	4282
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys 905 910	4330
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser 915 920 925 930	4378
GCA GAA GTC AAA TG GTACGTGTG GTCTCGAGAC TTCAGCAATA TTGACACATC Ala Glu Val Lys Trp 935	4432
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys 940 945 950	4480
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr 955 960 965	4528
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu 970 975 980	4576
CAT AGA AGA ATA GCT GAT TAATGTCAATT TTCAATTTAT TATATACATC His Arg Arg Ile Ala Asp 985	4624
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC	4684
ATACTATAGG ATTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC	4744
TTTATCCTTA TACTTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCA	4804
TTAAACGGGA GTGGTTAAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA	4864
ATAAGGAAAG TGGTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT	4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT	4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG	5044
TGACCGAATT TTGGTAAAAG CCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG	5104
AAAAGAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTT	5164

GTTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA	5224
TTCCGAAATA GCCAAATTC TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC	5284
TTATGAGGCT TCAAAACTC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT	5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTTG CAAAAAGAA AATATCATTG	5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT	5464
AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA	5524
GTTAAGTGAC CAAAGGTACC	5544

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Thr	Glu	His	His	Thr	Pro	Lys	Ser	Arg	Ile	Leu	Arg	Phe	Leu	Glu	1	5	10	15
Asn	Gln	Tyr	Val	Tyr	Leu	Cys	Thr	Leu	Asn	Asp	Tyr	Val	Gln	Leu	Val	20	25	30	
Leu	Arg	Gly	Ser	Pro	Ala	Ser	Ser	Tyr	Ser	Asn	Ile	Cys	Glu	Arg	Leu	35	40	45	
Arg	Ser	Asp	Val	Gln	Thr	Ser	Phe	Ser	Ile	Phe	Leu	His	Ser	Thr	Val	50	55	60	
Val	Gly	Phe	Asp	Ser	Lys	Pro	Asp	Glu	Gly	Val	Gln	Phe	Ser	Ser	Pro	65	70	75	80
Lys	Cys	Ser	Gln	Ser	Glu	Leu	Ile	Ala	Asn	Val	Val	Lys	Gln	Met	Phe	85	90	95	
Asp	Glu	Ser	Phe	Glu	Arg	Arg	Arg	Asn	Leu	Leu	Met	Lys	Gly	Phe	Ser	100	105	110	
Met	Asn	His	Glu	Asp	Phe	Arg	Ala	Met	His	Val	Asn	Gly	Val	Gln	Asn	115	120	125	
Asp	Leu	Val	Ser	Thr	Phe	Pro	Asn	Tyr	Leu	Ile	Ser	Ile	Leu	Glu	Ser	130	135	140	
Lys	Asn	Trp	Gln	Leu	Leu	Leu	Glu	Ile	Ile	Gly	Ser	Asp	Ala	Met	His	145	150	155	160
Tyr	Leu	Leu	Ser	Lys	Gly	Ser	Ile	Phe	Glu	Ala	Leu	Pro	Asn	Asp	Asn	165	170	175	
Tyr	Leu	Gln	Ile	Ser	Gly	Ile	Pro	Leu	Phe	Lys	Asn	Asn	Val	Phe	Glu	180	185	190	

Glu Thr Val Ser Lys Lys Arg Lys Arg Thr Ile Glu Thr Ser Ile Thr
 195 200 205
 Gln Asn Lys Ser Ala Arg Lys Glu Val Ser Trp Asn Ser Ile Ser Ile
 210 215 220
 Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser Tyr Lys Lys Phe Lys Gln
 225 230 235 240
 Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr Val His
 245 250 255
 Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile Asn Ala
 260 265 270
 Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser Gln Ser
 275 280 285
 Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile Glu Gln
 290 295 300
 Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr Asn His
 305 310 315 320
 Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu Ser Tyr
 325 330 335
 Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile Leu Val
 340 345 350
 Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe Glu Ile
 355 360 365
 Ile Leu Lys Asp Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser
 370 375 380
 Phe Ser Leu His Tyr Leu Met Ser Asn Ile Lys Ile Ser Glu Ile Glu
 385 390 395 400
 Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys Met Cys Leu Ser Asp
 405 410 415
 Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe Ile Tyr Trp Leu Tyr
 420 425 430
 Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu
 435 440 445
 Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
 450 455 460
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
 465 470 475 480
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
 485 490 495
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
 500 505 510
 Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
 515 520 525

Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
 530 535 540
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
 545 550 555 560
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
 565 570 575
 His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
 580 585 590
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 595 600 605
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
 610 615 620
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
 625 630 635 640
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
 645 650 655
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
 660 665 670
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
 675 680 685
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
 690 695 700
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 705 710 715 720
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val
 725 730 735
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 740 745 750
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 755 760 765
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser
 770 775 780
 Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met
 785 790 795 800
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu
 805 810 815
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu
 820 825 830
 Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser
 835 840 845
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser
 850 855 860

Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys
 865 870 875 880
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro
 885 890 895
 Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile
 900 905 910
 Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu
 915 920 925
 Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly
 930 935 940
 Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr
 945 950 955 960
 Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu
 965 970 975
 Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp
 980 985

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe
 1 5 10 15
 Tyr Arg Lys Ser Val Trp Ser Lys
 20

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
 1 5 10 15
 Val Arg Gln His Arg Glu Ala

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
1           5           10           15
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
           20           25

```

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly
1           5           10           15
Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
           20           25

```

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8

(ix) FEATURE:

(B) LOCATION: 10..11

```
/product="OILSEK"
/note="Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"
```

(A) NAME/KEY: Modified-site

(B) LOCATION: 12

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 13

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 21

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(A) NAME/KEY: Modified-site

(B) LOCATION: 25

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 28..29

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(A) NAME/KEY: Modified-site

(B) LOCATION: 31

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20 25 30

91

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29..30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
20 25 30
Xaa Xaa Trp
35

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20 25 30
Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
35 40

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr

(2) INFORMATION FOR SEQ ID NO:121:

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

(2) INFORMATION FOR SEQ ID NO:122:

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

(2) INFORMATION FOR SEQ ID NO:123:

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
 1 5 10 15
Xaa

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa
 1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Phe Tyr Xaa Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Phe Phe Tyr Val Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TTYTTYTAYG TNACNGA

17

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TCNGTNACRT ARAARAA

17

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

MGNTTYATHC CNAARCC

17

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GGYTTNGGDA TRAANC

16

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala Tyr Asp Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCNTAYGAYA CNAT

14

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TANGTRTCRT ANGC

14

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

SWNCCYTGNG GDATNCC

17

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Leu Val Asp Asp Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

YTNGTNGAYG AYTYYT

17

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asp Asp Phe Leu Leu Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GTNACNARNA RRAARTCRTC

20

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GTGAAGGCAC TGTTACGCG

19

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CGCGTGGGTG AGGTGAGGTG

20

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CTGTGCTGGG CCTGGACGAT A

21

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

AGCTTGTTCT CCATGTCGCC GTAG

24

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GTGGATGATT TCTTGTGG

19

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGACCCCAGG AGTGGCACG 19

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TCAAGCTGAC TCGACACCG 19

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CGGCGTGACA GGGCTGC 17

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GCTGAAGGCT GAGTGTCC 18

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TTTCCGTGTT GAGTGTTC

19

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTCACCGTGT TGGGCAGG

18

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GCTACCTGCC CAACACGG

18

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GCGCGAAGAA CGTGCTGG

18

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CACTGCTCCT TGTCGCCTG

19

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TTCCCAAGGA CTTTGTTC

19

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TGTTCTCAA GACGCACTG

19

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TACTGCGTGC GTCGGTATG

19

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGTCTTGCGG CTGAAGTGT

19

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TGGTTCACCT GCTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GTGGTTTCTG TGTGGTGTG

19

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GACACCACAC AGAAACCAC

19

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GTGCCAGCAG GTGAACCAG

19

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GCAGTGCGTC TTGAGGAGC

19

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

TGGAACCATA GCGTCAGGGA G

21

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGCCTCCCTG ACGCTATGGT T

21

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCKCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GCTCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ACGCCGAGAC CAAGCACTTC

20

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CCAAAGAGGT GGCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

AAGGCCAGCA CGTTCTTCGC

20

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

CACGTTCTGTG CGGCGCCTG

19

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCTTCACCAC CAGCGTGCG

19

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GGCGACGACG TGCTGGTTC

19

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GGCTCAGGGG CAGCGCCAC

19

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CTGGCAGGTG TACGGCTTC

19

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCGTGGACCG AGTGACCGTG GTTTC

25

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GACGTGGTGG CCGCGATGTG G

21

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAAGTCTGCC GTTGCCCAAG AG

22

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GACACCACAC AGAAACCACG GTCAC

25

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:
CGCCCCCTCC TTCCGCCAGG T

21

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:
CGAAGCCGAA GGCCAGCACG TTCTT

25

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:
GGTGGCCCGA GTGCTGCAGA GG

22

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:
GTAGCTGCGC ACGCTGGTGG TGAAG

25

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TGGGCGACGA CGTGCTGGTT CA

22

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TATGGTTCCA GGCCCGTTTCG CATCC

25

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCAGCTGCGC CTACCAGGTG TGC

23

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGCCTCCCTG ACGCTATGGT TCCAG

25

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:
 GGTGCTGCCG CTGGCCACGT TCG 23

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:
 TCCCAGGGCA CGCACACCAG GCACT 25

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:
 GTACAGGGCA CACCTTTGGT CACTC 25

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:
 TCGACGACGT ACACACTCAT CAGCC 25

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

AGCGGCAGCA CCTCGCGGTA GTGGC

25

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCACCAGCTC CTTCAGGCAG GACAC

25

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CCAGGGCTTC CCACGTGCGC AGCAG

25

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CGCACGAACG TGGCCAGCGG CAGCA

25

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TGACCGTGGT TTCTGTGTGG TGT

23

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCCTCTTCAA GTGCTGTCTG ATTCC

25

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATCGCGGCCA CCACGTCCCT

20

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TGCTCCAGAC ACTCGGCCGG TAGAA

25

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ACGAAGCCGT ACACCTGCC

19

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

CGACATCCCT GCGTTCTTGG CTTTC

25

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CACTGCTGGC CTCATTCAGG G

21

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:
CACTGCTGGC CTCATTCAGG G

21

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:
GCAGCCATAC TCAGGGACAC

20

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
CCATCCTCTC CACGCTGCTC

20

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
GCGATGACCT CCGTGAGCCT G

21

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:
CCCAGGACAG GCTCACGGA 19

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:
CCTCTTCAAG TGCTGTCTGA TTCC 24

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:
CAGCTCGACG ACGTACACAC TCATC 25

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:
CTGACGTCCA GACTCCGCTT CAT 23

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:
GACCTGAGCA GCTCGACGAC GTACACACTC ATC 33

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:
GTCGTCGAGC TGCTCAGGTC 20

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:
AGCACGCTGA ACAGTGCCTT 20

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:
GACCTGAGCA GCTCGACGAC 20

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

AAGGCACTGT TCAGCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

CGGCCGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGATGAAGCG GAGTCTGGA

19

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ATGGATCCGT CGTCGAGCTG CTCAGGTCT

29

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ATCAGCTGAG CACGCTGAAC AGTGCCTTC

29

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GTCTCCGTGA CATAAAAGAA AGAC

24

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GCCAAGTTCC TGCACTGGCT

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /mod_base= OTHER
 /note= "N = guanosine substituted by two
 biotin groups"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

NCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GTCAAGATGC CTGAGATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCTTAGCTT GTGGGGGTGT CA

22

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:
GCTGCGTCCT GCTGCGCACG T 21

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:
CAGCGGGGAG CGCGCGGCAT C 21

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:
TGGGCCACCA GCGCGCGGAA A 21

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:
CGGCCGCAGC CCGTCAGGCT TGGGG 25

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

CCGACAGCTC CCGCAGCTGC ACCC

24

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CGTACACACT CATCAGCCAG TGCAGGAAGT TGGC

34

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

CGCGCCCGCT CGTAGTTGAG CACGCTGAAC AGTGCCTTC

39

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GCGGAGTCTG GACGTCAGCA GGGCGGGCCT GGCTTCCCG

39

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

ATTGACCCA CAGGGACCCC CATCCAG

27

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

ATGACCGCCC TCCTCGTGAG

20

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GCCACCCCCG CGATGCC

17

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

AGCCCTGGCC CCGGCCA

17

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TCCCACGTGC GCAGCAG

17

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

AGCAGGACGC AGCGCTG

17

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

CGCGGTAGTG GCTGCGCAGC AGGGAGCGCA CGGC

34

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CCAGGGCTTC CCACGTGCGC AGCAGGACGC AGCGC

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:
CACTGCTGGC CTCATTCAGG G

21

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:
GCAGCCATAC TCAGGGACAC

20

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
CCATCCTCTC CACGCTGCTC

20

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
GCGATGACCT CCGTGAGCCT G

21

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CCCAGGACAG GCTCACGGA

19

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CCTCTTCAAG TGCTGTCTGA TTCC

24

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CAGCTCGACG ACGTACACAC TCATC

25

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CTGACGTCCA GACTCCGCTT CAT

23

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GACCTGAGCA GCTCGACGAC GTACACACTC ATC

33

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GTCGTCGAGC TGCTCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGCACGCTGA ACAGTGCCTT

20

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GACCTGAGCA GCTCGACGAC

20

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

AAGGCACTGT TCAGCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

CGGCCGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGATGAAGCG GAGTCTGGA

19

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ATGGATCCGT CGTCGAGCTG CTCAGGTCT

29

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ATCAGCTGAG CACGCTGAAC AGTGCCTTC

29

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GTCTCCGTGA CATAAAAGAA AGAC

24

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GCCAAGTTCC TGCACTGGCT

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /mod_base= OTHER
 /note= "N = guanosine substituted by two
 biotin groups"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

NCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GTCAAGATGC CTGAGATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCTTAGCTT GTGGGGGTGT CA

22

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:
GCTGCGTCCT GCTGCGCACG T 21

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:
CAGCGGGGAG CGCGCGGCAT C 21

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:
TGGGCCACCA GCGCGCGGAA A 21

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:
CGGCCGCGAGC CCGTCAGGCT TGGGG 25

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

CCGACAGCTC CCGCAGCTGC ACCC

24

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CGTACACACT CATCAGCCAG TGCAGGAACT TGGC

34

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

CGCGCCCGCT CGTAGTTGAG CACGCTGAAC AGTGCCTTC

39

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GCGGAGTCTG GACGTCAGCA GGGCGGGCCT GGCTTCCCG

39

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

ATTTGACCCA CAGGGACCCC CATCCAG

27

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

ATGACCGCCC TCCTCGTGAG

20

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GCCACCCCCG CGATGCC

17

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

AGCCCTGGCC CCGGCCA

17

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TCCCACGTGC GCAGCAG

17

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

AGCAGGACGC AGCGCTG

17

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

CGCGGTAGTG GCTGCGCAGC AGGGAGCGCA CGGC

34

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CCAGGGCTTC CCACGTGCGC AGCAGGACGC AGCGC

35

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

CTAGTCTAGA TCRCTAGCGT AATCTGGAAC ATCGTATGGG TRTCCAGGAT GGTCTTGAAG 60

TC 62

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TACCATGGGC TACCCATACG ACGTTCCAGA TTACGCTCA 39

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

TATGAGCGTA ATCTGGAACG TCGTATGGGT AGCCCATGG 39

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GTGTACGTCG TCGAGCTCCT CAGGTCTGCC TTTTATGTCA CGGAG

45

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GTGTACGTCG TCGAGCTCCT CAGGTCTTTC GCTTATGTCA CGGAGACC

48

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CCTCAGGTCT TTCTTTGCTG TCACGGAGAC AACGTTTCAA AAGAACAG

48

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GGTCTTTCTT TTATGTCGCG GAGACAACGT TTCAAAGAA CAG

43

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CTTCTCTTTTA TGTCACGGCG ACAACGTTTC AAAAGAACA

39

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

ATGAGTGTGT ACGTCGTCGA GCTCCTCAGG TCTACCACGC AAAAGAACAG GCTCTTTTTC

60

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GGCTGATGAG TGTGTACGTC GTCGA

25

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

ACGTGGTCTC CGTGACATAA AAGAA

25

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:
AGGTCTTTCT TTTATGTCAC GGA 23

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:
CACAGACCCC CGTCGCCTGG TC 22

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:
CGGAGTCTGG ACGTCAGCAG GGC 23

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:
CGCGGATCCG TAACTAAAAT GCCGCGCGCT CCCCCTGC 39

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

CCGGAATTCG TTAGTTACTT ACAAAGAGGT GGCTTCTTCG GC

42

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

CGCGGATCCG TAACTAAAGC CACCTCTTTG GAGGGTGCG

39

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CCGGAATTCG TTAGTTACTT AAGACCTGAG CAGCTCGACG AC

42

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

CGCGGATCCG TAACTAAAAT GAGTGTGTAC GTCGTCGAG

39

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:
 CCGGAATTCG TTAGTTACTT AGATCCCCTG GCACTGGACG 40

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:
 CGCGGATCCG TAACTAAAT CCCGCAGGGC TCCATCCTC 39

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:
 CCGGAATTCG TTAGTTACTT AGTCCAGGAT GGTCTTGAAG TC 42

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:
 GGCATCGCGG GGGTGGCCGG G 21

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GGACACCTGG CGGAAGGAGG G

21

- (2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GCGTGCCAGC AGGTGAACCA G

21

- (2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

CTCAGGGGCA GCGCCACGCC T

21

- (2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

AGGTGGCTTC TTCGGCGGGT C

21

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GGACAAGGCG TGTCCCAGGG A

21

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GCTGGGGTGA CCGCAGCTCG C

21

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GATGAACTTC TTGGTGTTC T

21

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GTGCGCCAGG CCCTGTGGAT A

21

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GCCCATGGGC GGCCTTCTGG A

21

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAGGCCACTG CTGGCCTCAT T

21

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GGGTGAGGTG AGGTGTCACC A

21

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GCTGCAGCAC ACATGCGTGA AACCTGTACG C

31

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GACGCGCAGG AAAAATGTGG G

21

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

CCGAGCGCCA GCCTGTGGGG A

21

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

CAGCGGGGAG CGCGCGGCAT C

21

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

CAGCACCTCG CGGTAGTGGC T

21

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

TCAAGCCAAA CCTGAATCTG AG

22

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CCCGAGTGAA TCTTTCTACG C

21

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GTCTCTGGCA GTTCTCAT CCC

23

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

TTTAGGCATC CTCCAAGCA CA

22

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

TTAGGGTTAG

10

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

TTAGGGTTAG GGTTAGG

18

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

GTTAGGGTTA GGGTTAGG

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: repeat_unit
(B) LOCATION: 1..6
(D) OTHER INFORMATION: /note= "sequence (CCCTAA)-n, where n is at least 1, or at least 3, or at least 10 or more"

CCCTAACCCT AACCTAACC CTAACCCTAA CCCTAACCCT AACCTAACC CTAACCCTAA

60

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "non-telomeric nucleotide
sequence, (N)-n, where n is 8-20,
or 6-30"

NNNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAG

34

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (N)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

NNNNNNNNNNNN NNNNNNNNNNNN NNNNNNNNNNNN AGGG

34

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (N)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

NNNNNNNNNNNN NNNNNNNNNNNN NNNNNNNNNNNN TTAGGGTTAG

40

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (N)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

NNNNNNNNNNNN NNNNNNNNNNNN NNNNNNNNNNNN TTAGGGTTAG GGTTAG

46

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "non-telomeric nucleotide
sequence, (N)-n, where n is 8-20,
or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AG

52

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "non-telomeric nucleotide
sequence, (N)-n, where n is 8-20,
or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AGGGTTAG

58

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

TAGGGATTAG

10

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 3'-deoxyguanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

TTAGGGTTAG GGTAN

16

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "sequence (TTAGGG)-n, where n
is 1-10, or typically 3-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

TTAGGGTTAG GGTAGGGTT AGGGTTAGGG TTAGGGTTAG GGTAGGGTT AGGGTTAGGG

60

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GGCACTGGAC GTAGGACGTG

20

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

CGGAAGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

CTCAGACACC ATGGGGAAGG TGA

23

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

ATGATCTTGA GGCTGTTGTC ATA

23

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

26

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

CCCCCGCCG	CCCCCTCCTT	CCGCCAGGTG	GGCTCCCCG	GGGTCGGCGT	CCGGCTGGGG	60
TTGAGGGCGG	CCGGGGGGAA	CCAGCGACAT	GCGGAGAGCA	GCGCAGGCGA	CTCAGGGCGC	120
TTCCCCCGCA	GGTGTCTGTC	CTGAAGGAGC	TGGTGGCCCCG	AGTGCTGCAG		170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met	Ser	Asp	Lys	Ile	Ile	His	Leu	Thr	Asp	Asp	Ser	Phe	Asp	Thr	Asp
1				5					10					15	
Val	Leu	Lys	Ala	Asp	Gly	Ala	Ile	Leu	Val	Asp	Phe	Trp	Ala	His	Trp
			20					25					30		
Cys	Gly	Pro	Cys	Lys	Met	Ile	Ala	Pro	Ile	Leu	Asp	Glu	Ile	Ala	Asp
		35					40					45			
Glu	Tyr	Gln	Gly	Lys	Leu	Thr	Val	Ala	Lys	Leu	Arg	Ile	Asp	His	Asn

50					55					60					
Pro	Gly	Thr	Ala	Pro	Lys	Tyr	Gly	Ile	Arg	Gly	Ile	Pro	Thr	Leu	Leu
65					70					75					80
Leu	Phe	Lys	Asn	Gly	Glu	Val	Ala	Ala	Thr	Lys	Val	Gly	Ala	Leu	Ser
				85					90					95	
Lys	Gly	Gln	Leu	Lys	Glu	Phe	Leu	Asp	Ala	Asn	Leu	Ala	Gly	Ser	Gly
			100					105					110		
Ser	Gly	Asp	Asp	Asp	Asp	Lys	Val	Pro	Met	His	Glu	Leu	Glu	Ile	Phe
		115					120					125			
Glu	Phe	Ala	Ala	Ala	Ser	Thr	Gln	Arg	Cys	Val	Leu	Leu	Arg	Thr	Trp
	130					135					140				
Glu	Ala	Leu	Ala	Pro	Ala	Thr	Pro	Ala	Met	Pro	Arg	Ala	Pro	Arg	Cys
145					150					155					160
Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	His	Tyr	Arg	Glu	Val	Leu	Pro
				165					170					175	
Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	Leu	Val
			180					185					190		
Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	Cys	Leu
		195					200					205			
Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Pro	Ala	Ala	Pro	Ser	Phe
	210					215					220				
Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg
225					230					235					240
Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu
				245					250					255	
Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val
		260					265						270		
Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly
		275					280					285			
Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His
	290					295					300				
Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala
305					310					315					320
Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln
				325					330					335	
Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys
			340					345					350		
Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly
		355					360					365			
Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser
	370					375					380				

Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 385 390 395 400
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 405 410 415
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 420 425 430
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 435 440 445
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 450 455 460
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 465 470 475 480
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 485 490 495
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 500 505 510
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 515 520 525
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 530 535 540
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 545 550 555 560
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 565 570 575
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 580 585 590
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 595 600 605
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 610 615 620
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 625 630 635 640
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 645 650 655
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 660 665 670
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 675 680 685
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 690 695 700
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 705 710 715 720

Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
725 730 735
Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
740 745 750
Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
755 760 765
Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
770 775 780
Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
785 790 795 800
Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
805 810 815
Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
820 825 830
Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
835 840 845
Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
850 855 860
Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
865 870 875 880
Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
885 890 895
Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
900 905 910
Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
915 920 925
Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
930 935 940
Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
945 950 955 960
Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
965 970 975
Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
980 985 990
Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
995 1000 1005
Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
1010 1015 1020
Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
1025 1030 1035 1040
Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
1045 1050 1055

Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 1060 1065 1070
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1075 1080 1085
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 1090 1095 1100
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1105 1110 1115 1120
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1125 1130 1135
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1140 1145 1150
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1155 1160 1165
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1170 1175 1180
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1185 1190 1195 1200
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1205 1210 1215
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1220 1225 1230
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1235 1240 1245
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1250 1255 1260
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1265 1270 1275 1280
 Lys Thr Ile Leu Asp
 1285

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Gly Ser Val Thr Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5				10						15		
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20				25						30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170					175		
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Ile	Pro	Gln	Gly	
225					230					235					240	
Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	
				245					250					255		
Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	

260					265					270					
Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	Thr
	275						280					285			
Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val
	290					295					300				
Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu
305					310					315					320
Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	Trp
				325					330					335	
Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr
			340					345					350		
Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Val	Thr	Phe	Asn	Arg
		355					360					365			
Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu
	370					375					380				
Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu
385					390				395						400
Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln	Ala	Tyr
				405					410					415	
Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	Phe	His	Gln	Gln	Val	Trp
			420					425					430		
Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile	Ser	Asp	Thr	Ala	Ser	Leu
		435					440					445			
Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala	Gly	Met	Ser	Leu	Gly	Ala
	450					455					460				
Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro	Ser	Glu	Ala	Val	Gln	Trp	Leu	Cys
465					470				475					480	
His	Gln	Ala	Phe	Leu	Leu	Lys	Leu	Thr	Arg	His	Arg	Val	Thr	Tyr	Val
			485					490					495		
Pro	Leu	Leu	Gly	Ser	Leu	Arg	Thr	Ala	Gln	Thr	Gln	Leu	Ser	Arg	Lys
			500					505					510		
Leu	Pro	Gly	Thr	Thr	Leu	Thr	Ala	Leu	Glu	Ala	Ala	Ala	Asn	Pro	Ala
		515					520					525			
Leu	Pro	Ser	Asp	Phe	Lys	Thr	Ile	Leu	Asp						
	530					535									

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5					10					15		
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170					175		
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	His	His	His	His	His	His	
225					230					235					240	
His	His	Gly	Ser	Val	Thr	Lys	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	
				245					250					255		
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	
			260					265					270			
Phe	Phe	Tyr	Arg	Pro	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	
		275					280					285				
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	
	290					295					300					

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 305 310 315 320
 Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 325 330 335
 Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 340 345 350
 Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 355 360 365
 Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 370 375 380
 Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 385 390 395 400
 Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 405 410 415
 Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 420 425 430
 Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 435 440 445
 Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 450 455 460
 Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 465 470 475 480
 Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 485 490 495
 Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 500 505 510
 Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 515 520 525
 Gly Ile
 530

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Ser Val Tyr
 225 230 235 240
 Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe
 245 250 255
 Gln Lys Asn Arg Leu Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu
 260 265 270
 Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu
 275 280 285
 Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu
 290 295 300
 Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro
 305 310 315 320
 Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu
 325 330 335
 Lys Arg Ala Glu Arg Leu Thr Ser Arg Lys Ala Leu Phe Ser Val Leu
 340 345 350

Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu
 355 360 365
 Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val
 370 375 380
 Arg Ala Gln Asp Pro Pro Pro Glu Tyr Phe Val Lys Val Asp Val Thr
 385 390 395 400
 Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 405 410 415
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 420 425 430
 Val Gln Lys Ala Ala His Gly Val Arg Lys Ala Phe Lys Ser His Val
 435 440 445
 Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His
 450 455 460
 Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser
 465 470 475 480
 Ser Ser Leu Asn Glu Ala Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 485 490 495
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 500 505 510
 Gln Gly Ile
 515

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 514 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	85	90	95
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	100	105	110
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	115	120	125
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	130	135	140
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	145	150	155
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	165	170	175
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Ala	Thr	Ser	Leu	225	230	235
Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	245	250	255
Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	260	265	270
Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	275	280	285
Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	290	295	300
Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	305	310	315
Leu	Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	325	330	335
Leu	Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	340	345	350
Gly	Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	355	360	365
Pro	Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	370	375	380
Lys	Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	385	390	395
Arg	Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	405	410	415

Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 420 425 430
 Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 435 440 445
 Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 450 455 460
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 465 470 475 480
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 485 490 495
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 500 505 510
 Arg Ser

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 517 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp

145		150		155		160
Val Val Leu Tyr	Met Asp Pro Met Cys	Leu Asp Ala Phe Pro Lys Leu				
	165	170			175	
Val Cys Phe Lys	Lys Arg Ile Glu Ala	Ile Pro Gln Ile Asp Lys Tyr				
	180	185			190	
Leu Lys Ser Ser	Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala					
	195	200			205	
Thr Phe Gly Gly	Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg					
	210	215			220	
Gly Ser Arg Arg	Ala Ser Val Gly Ser Val Thr Lys Met Pro Arg Ala					
	225	230			235	240
Pro Arg Cys Arg	Ala Val Arg Ser Leu Leu Ser His Tyr Arg Glu Val					
	245	250			255	
Leu Pro Leu Ala	Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg					
	260	265			270	
Leu Val Gln Arg	Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln					
	275	280			285	
Cys Leu Val Cys	Val Pro Trp Asp Ala Arg Pro Pro Ala Ala Pro Ser					
	290	295			300	
Phe Arg Gln Val	Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln					
	305	310			315	320
Arg Leu Cys Glu	Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala					
	325	330			335	
Leu Leu Asp Gly	Ala Arg Gly Gly Pro Pro Glu Ala Thr Thr Ser Val					
	340	345			350	
Arg Ser Tyr Leu	Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly					
	355	360			365	
Ala Trp Gly Leu	Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His					
	370	375			380	
Leu Leu Ala Arg	Cys Ala Leu Phe Val Leu Val Ala Pro Cys Ala Tyr					
	385	390			395	400
Gln Val Cys Gly	Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala					
	405	410			415	
Arg Pro Pro Pro	His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu					
	420	425			430	
Arg Ala Trp Asn	His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu					
	435	440			445	
Pro Ala Pro Gly	Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu					
	450	455			460	
Pro Leu Pro Lys	Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg					
	465	470			475	480

Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly
485 490 495
Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu
500 505 510
Glu Ala Thr Ser Leu
515

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

CCGGCCACCC CCCATATGCC GCGCGCTCCC

30

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Asn Ser Ala Val Asp
1 5

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

35					40					45					
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro
50					55					60					
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu
65					70					75					80
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val
				85					90					95	
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro
			100					105					110		
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr
			115				120					125			
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val
					135					140					
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val
145				150						155					160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr
				165					170					175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly
			180					185					190		
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg
			195				200					205			
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg
			210			215					220				
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg
225				230						235					240
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp
				245					250					255	
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val
			260				265						270		
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala
			275				280					285			
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His
			290			295					300				
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro
305				310						315					320
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly
				325					330					335	
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro
			340					345					350		
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser
			355				360					365			

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700

Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile
705					710					715					720
Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln
				725					730					735	
Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His
			740					745					750		
Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp
		755					760					765			
Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser
	770					775					780				
Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu
785					790					795					800
Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His
				805					810					815	
Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro
			820					825					830		
Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp
		835					840					845			
Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu
	850					855					860				
Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala
865					870					875					880
Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys
				885					890					895	
Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu
			900					905					910		
Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe
		915					920					925			
Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser
	930					935					940				
Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe
945					950					955					960
Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly
				965					970					975	
Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn
			980					985					990		
Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln
		995					1000					1005			
Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	Phe	His	Gln	Gln
	1010					1015					1020				
Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile	Ser	Asp	Thr	Ala
1025					1030					1035					1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp Leu Glu Gln Lys
 1125 1130 1135
 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 1140 1145 1150
 His His

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Pro Arg Gly Ser His His His His His His Gly Met Ala Ser Met
 1 5 10 15
 Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Leu
 20 25 30
 Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met Glu Phe Ala Ala Ala
 35 40 45
 Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro
 50 55 60
 Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser
 65 70 75 80
 Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val
 85 90 95
 Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro
 100 105 110
 Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp
 115 120 125
 Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys

130					135					140					
Leu 145	Lys	Glu	Leu	Val	Ala 150	Arg	Val	Leu	Gln	Arg 155	Leu	Cys	Glu	Arg	Gly 160
Ala	Lys	Asn	Val	Leu 165	Ala	Phe	Gly	Phe	Ala 170	Leu	Leu	Asp	Gly	Ala	Arg 175
Gly	Gly	Pro	Pro 180	Glu	Ala	Phe	Thr	Thr 185	Ser	Val	Arg	Ser	Tyr	Leu	Pro 190
Asn	Thr	Val	Thr 195	Asp	Ala	Leu	Arg	Gly 200	Ser	Gly	Ala	Trp	Gly	Leu	Leu 205
Leu	Arg 210	Arg	Val	Gly	Asp	Asp 215	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys 220
Ala 225	Leu	Phe	Val	Leu	Val 230	Ala	Pro	Ser	Cys	Ala 235	Tyr	Gln	Val	Cys	Gly 240
Pro	Pro	Leu	Tyr	Gln 245	Leu	Gly	Ala	Ala	Thr 250	Gln	Ala	Arg	Pro	Pro	Pro 255
His	Ala	Ser	Gly 260	Pro	Arg	Arg	Arg	Leu 265	Gly	Cys	Glu	Arg	Ala	Trp	Asn 270
His	Ser	Val	Arg 275	Glu	Ala	Gly	Val 280	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly 285
Ala	Arg 290	Arg	Arg	Gly	Gly	Ser 295	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys 300
Arg 305	Pro	Arg	Arg	Gly	Ala 310	Ala	Pro	Glu	Pro	Glu 315	Arg	Thr	Pro	Val	Gly 320
Gln	Gly	Ser	Trp	Ala 325	His	Pro	Gly	Arg	Thr 330	Arg	Gly	Pro	Ser	Asp	Arg 335
Gly	Phe	Cys	Val 340	Val	Ser	Pro	Ala	Arg 345	Pro	Ala	Glu	Glu	Ala	Thr	Ser 350
Leu	Glu	Gly	Ala 355	Leu	Ser	Gly	Thr 360	Arg	His	Ser	His	Pro	Ser	Val	Gly 365
Arg	Gln 370	His	His	Ala	Gly	Pro 375	Pro	Ser	Thr	Ser	Arg 380	Pro	Pro	Arg	Pro 385
Trp 385	Asp	Thr	Pro	Cys	Pro 390	Pro	Val	Tyr	Ala	Glu 395	Thr	Lys	His	Phe	Leu 400
Tyr	Ser	Ser	Gly	Asp 405	Lys	Glu	Gln	Leu	Arg 410	Pro	Ser	Phe	Leu	Leu	Ser 415
Ser	Leu	Arg	Pro 420	Ser	Leu	Thr	Gly	Ala 425	Arg	Arg	Leu	Val	Glu	Thr	Ile 430
Phe	Leu	Gly 435	Ser	Arg	Pro	Trp	Met 440	Pro	Gly	Thr	Pro	Arg 445	Arg	Leu	Pro 450
Arg 450	Leu	Pro	Gln	Arg	Tyr	Trp 455	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu 460

Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His
 465 470 475 480
 Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg
 485 490 495
 Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
 500 505 510
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
 515 520 525
 Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
 530 535 540
 Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
 545 550 555 560
 Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu
 565 570 575
 Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
 580 585 590
 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile
 595 600 605
 Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu
 610 615 620
 Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg
 625 630 635 640
 Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 645 650 655
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala
 660 665 670
 Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 675 680 685
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 690 695 700
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 705 710 715 720
 Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 725 730 735
 Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
 740 745 750
 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
 755 760 765
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
 770 775 780
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 785 790 795 800

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 805 810 815
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 820 825 830
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 835 840 845
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 850 855 860
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 865 870 875 880
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 885 890 895
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 900 905 910
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 915 920 925
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 930 935 940
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 945 950 955 960
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 965 970 975
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 980 985 990
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 995 1000 1005
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 1010 1015 1020
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 1025 1030 1035 1040
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 1045 1050 1055
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 1060 1065 1070
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 1075 1080 1085
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1090 1095 1100
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1105 1110 1115 1120
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1125 1130 1135

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
1140 1145 1150
His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
1155 1160 1165
Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
1170 1175 1180
Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1185 1190 1195 1200

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15
Ser Tyr Ile Tyr Ala Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met
20 25 30
Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
35 40 45
Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
50 55 60
Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
65 70 75 80
Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
85 90 95
Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
100 105 110
Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
115 120 125
Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
130 135 140
Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
145 150 155 160
Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
165 170 175
Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
180 185 190

Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 195 200 205
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
 210 215 220
 Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 225 230 235 240
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 245 250 255
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 260 265 270
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 275 280 285
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 290 295 300
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 305 310 315 320
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 325 330 335
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 340 345 350
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 355 360 365
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 370 375 380
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 385 390 395 400
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 405 410 415
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 420 425 430
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 435 440 445
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 450 455 460
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 465 470 475 480
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 485 490 495
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 500 505 510
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 515 520 525

Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 530 535 540
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 545 550 555 560
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 565 570 575
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 580 585 590
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 595 600 605
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 610 615 620
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 625 630 635 640
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 645 650 655
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 660 665 670
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 675 680 685
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 690 695 700
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 705 710 715 720
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 725 730 735
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 740 745 750
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 755 760 765
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 770 775 780
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 785 790 795 800
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 805 810 815
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 820 825 830
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 835 840 845
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 850 855 860

Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 865 870 875 880
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 885 890 895
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 900 905 910
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 915 920 925
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 930 935 940
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 945 950 955 960
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 965 970 975
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 980 985 990
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 995 1000 1005
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1010 1015 1020
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1025 1030 1035 1040
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1045 1050 1055
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1060 1065 1070
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1075 1080 1085
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1090 1095 1100
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1105 1110 1115 1120
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1125 1130 1135
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1140 1145 1150
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1155 1160 1165
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1170 1175 1180
 Lys Thr Ile Leu Asp
 1185

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

TGCGCACGTG GGAAGCCCTG GCAGATCTGA ATTCCACCAT GCCGCGCGCT CCCCCTG 58

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

CTGCCCTCAG ACTTCAAGAC CATCCTGGAC TACAAGGACG ACGATGACAA ATGAATTCAG 60
ATCTGCGGCC GCCACCGCGG TGGAGCTCCA GC 92

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGGGACGGGC TGCTCCTGCG TTTGGTGGAC GCGTTCTTGT TGGTGACACC TCACCTCACC 60

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

ATTCCGTCGA GCAGAGTTAG GGTTAGGGTT AGGGTTAGGG TTAGGGTTAG GGTTAGGGTT 60
AG 62

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGC 60
TCCCACGACG TAGTCCATGT TCAC 84

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GGGTCTAGAT CCGGAAGAGT GTCTGGAGCA AG 32

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGG 60
CGGCCTTCTG GACCACGGCA TACC 84

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GGTCTAGACG ATATCCACAG GGCCTGGCGC

30

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1407 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155				160		
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
			165					170						175		
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
		180						185					190			
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
		195					200						205			

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Arg Thr Gln Ile Ser Ser Ser Ser Phe Glu Phe Ala Ala Ala Ser
 245 250 255
 Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala
 260 265 270
 Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu
 275 280 285
 Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg
 290 295 300
 Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala
 305 310 315 320
 Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp
 325 330 335
 Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu
 340 345 350
 Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala
 355 360 365
 Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly
 370 375 380
 Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn
 385 390 395 400
 Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu
 405 410 415
 Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala
 420 425 430
 Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro
 435 440 445
 Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His
 450 455 460
 Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His
 465 470 475 480
 Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala
 485 490 495
 Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg
 500 505 510
 Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln
 515 520 525
 Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly
 530 535 540

Phe	Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	545	550	555	560
Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	565	570	575	
Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	580	585	590	
Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	595	600	605	
Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	610	615	620	
Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	625	630	635	640
Leu	Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	645	650	655	
Leu	Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	660	665	670	
Gly	Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	675	680	685	
Pro	Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	690	695	700	
Lys	Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	705	710	715	720
Arg	Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	725	730	735	
Tyr	Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	740	745	750	
Trp	Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	755	760	765	
Phe	Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	770	775	780	
Trp	Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	785	790	795	800
Val	Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	805	810	815	
Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	820	825	830	
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	835	840	845	
Phe	Phe	Tyr	Arg	Pro	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	850	855	860	
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	865	870	875	880

Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
885 890 895
Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
900 905 910
Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
915 920 925
Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
930 935 940
Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
945 950 955 960
Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
965 970 975
Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
980 985 990
Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
995 1000 1005
Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
1010 1015 1020
Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
1025 1030 1035 1040
Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
1045 1050 1055
Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
1060 1065 1070
Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
1075 1080 1085
Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
1090 1095 1100
Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys
1105 1110 1115 1120
Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly
1125 1130 1135
Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu
1140 1145 1150
Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu
1155 1160 1165
Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val
1170 1175 1180
Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His
1185 1190 1195 1200
Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu
1205 1210 1215

Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser
 1220 1225 1230
 Val Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys
 1235 1240 1245
 Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu
 1250 1255 1260
 Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu
 1265 1270 1275 1280
 Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe
 1285 1290 1295
 His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser
 1300 1305 1310
 Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly
 1315 1320 1325
 Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala
 1330 1335 1340
 Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His
 1345 1350 1355 1360
 Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr
 1365 1370 1375
 Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala
 1380 1385 1390
 Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1395 1400 1405

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Gly Ser Thr His Ile Ser His Ile Ser His Ile Ser His Ile Ser His
 1 5 10 15
 Ile Ser His Ile Ser His Ile Ser His Ile Ser
 20 25